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1: /SIDS1/gcgdata/hold-geneseq/geneseqp.emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp.emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/hold-geneseq/geneseqp.emb1/AA1982.DAT:*

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MHP3; antigen; vaccine; enzootic mycoplasma pneumonia; antibody; immunoassay; immunotherapy; anti-idiotypic antibody.

Mycoplasma hyopneumoniae MHP3 antigen

07-SEP-2001 AAU01859; AAU01859

(first entry)

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  AAU01860;
                          AAU01860 standard;
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Pred. No. 8.6e-163;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 19-21; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New apoprotein antigens encoded by \mathfrak{m}hp3 gene from Mycoplasma hyopneumoniae useful as a vaccine for treating or preventing
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ody; immunoassay; immunotherapy; anti-idiotypic antibody;
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                                                                                                                                                                                                                                                                                423 AA;
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16-SEP-1987;
11-DEC-1987;
04-JAN-1988;
16-MAR-1990;
02-OCT-1992;
Regression associated antigens (RAA's) are identified in material from neoplastic cells by their immunological reactivity with regression associated antibodies from the serum of patients
                                                      DNA encoding a regression-associated antigen from M. is used to obtain prods. for diagnosis, localisation of tumours % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                       07-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                   Disclosure; Figure
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DB; AAQ47816.
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87US-0097910.
87US-0131815.
88US-0138923.
90US-0474730.
92US-0956546.
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Best Local
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                                                                                                                                                                                      Cancer metastasis;
                                                                                                                                                                                                                                    06-OCT-1995
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Pred. No. 6.7e-48;
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RESULT
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Best Local Similarity
Matches 168; Conserv
                             AAP93343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ79124 encodes AAR67582 a protein involved in cancer metastasis which may be used for the study of metastaic mechanisms, and for clinical tests to determine the presence or absence of cancer
          01-AUG-1990
                                               AAP93343
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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N-PSDB; AAQ79124.
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                                               standard;
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Pred. No. 3.6e-47;
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Query Match
Best Local S
Matches 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour regression-associated antigens used in diagnostic tests, monitoring therapy in cancer patients
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N-PSDB; AAN90684.
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therapy monitoring; cancer therapy; Mycoplasma
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ykgisd-flgvsnstvadadkvkaqefln-atadfkkqiqanpt-nyksvlgipmlindn
                                         YLGIKDREVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEM-PDK
                                                                                                        DTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGK----KSATV 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFNQSGWEAI----QQLGALTG-GEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETTKEEKSADNONKOITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDN 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-097910
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY05332 standard;
                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the inflammatory cytokine of the invention. The inflammatory cytokine can be used in a drug, which useful for the treatment of thrombocytopaenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP11089582-A
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                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New inflammatory cytokine inducer gene and polypeptide - useful for treatment of thrombocytopaenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX33847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-SEP-1997;
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                                                                                                                                                                                                                                                                                                              Local Similarity
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                       FFTSILKNLGYSVFSVLSDL-----YTKKSNSRNLAGFEFGKKSATVYLGIKDRF
                                                                                                                                              ernqikiigidf dieteykw--fyslqfnikesafttgyaiaswlseq---deskrvva
                                                                                                                                                                                                              QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-281057/24.
iltsvlkhikqavyetlldlilekeegykpyvvkdkkadkkwshfgtq-----
                                              vinnvlsstpadvkynphvilsvagpat--fetvrlankgqyvigvosdqgmi--qdkdr
                                                                                              sfgggafpgvttfnegfakgilyynqkh--ksskiyhtspvkldsgf-----tagekmnt
                                                                                                                      VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ
                                                                                                                                                                      TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 194
                                                                                                                                                                                               kainkqtgieinnveps-snfesaynsalsaghkiwvlngfkhqqsikqy--idahreel 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 16-17; 22pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                               428
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                                                           -KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK 303
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                                                                                                                                                                                                                                                                                                            17.6%;
26.7%;
                                                                                                                                                                                                                                                                                                 ; 88
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                                                                                                                                                                                                                                                                                                           Score 379.5; DB 2
Pred. No. 4.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombocytopaenia; therapy
                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                 156;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                        Length 428;
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13 ADNONKQIT----DVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQ

Conservative

Indels

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80 68

SGWEAIQOLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIP 128 safealkainkqtgieinnveps-snfesaynsalsaghkixvlngfkhqqsikqy--id 137

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Query Match

Best Local Similarity

Matches 117; Conserv
                                                              This sequence is a membrane protein designated M161Ag. Oligonucleotide probes for the CDNA were designed from putative N-terminal M161Ag pept sequences isolated from P93 cells. M161Ag can be used in the developme of a leukaemia treating agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW22727 standard; Protein;
                                              Sequence
                                                                                                            Claim 1; Fig 1; 6pp; Japanese
                                                                                                                             Membrane protein M161Ag treating agent
                                                                                                                                                          N-PSDB; AAT75133
                                                                                                                                                                   WPI; 1997-369470/34.
                                                                                                                                                                                                      05-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Membrane protein M161Ag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW22727;
                                                                                                                                                                                   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                        358
                                                                                                                                                                                                                                                                                                          /note= "selenocysteine"
348
                                                                                                                                                                                                                                                                                                                           /note= "selenocysteine"
185
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        17.3%;
                                                                                                                                                                                                                                                                                                 "selenocysteine"
                                                                                                                                                                                                                                                                              "selenocysteine"
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                                                                                                                                        useful
; Score 372; DB 18;
; Pred. No. 1.9e-21;
88; Mismatches 167;
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                  Length 429;
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RESULT
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AAY81501 to AAY81679 represent specifically claimed protein sequences isolated from Streptococcus pneumoniae. AAA05407 to AAA05590 represent specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and in diagnostic assays. The nucleotide sequences can be used in vaccines and in diagnostic assays. The proteins and nucleotides can be useful for the detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection
                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-1998;
19-MAR-1999;
                                                                                                                                                                                                                                 New Streptococcal protein, useful as a vaccine, pneumococcal diseases and for screening agents or inhibiting expression of the protein
                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                  WPI; 2000-195300/17.
                                                                                                                                                                                                                                                                                                                                  Gilbert CFG,
                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumococcal disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae type 4 protein sequence
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99US-0125164.
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RESULT
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និង្គិ
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         Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                           WPI; 1998-272224/24.
N-PSDB; AAV27326.
                                                                                                                                                  31-OCT-1996;
                                                                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                   Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                              AAW55066 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and meningitis. \mbox{AAA05591} to \mbox{AAA05614} represent primers exemplification of the present invention.
                                                                                                 Choi GH,
                                                                                                                                                                           30-OCT-1997;
                                                                                                                                                                                                    07-MAY-1998.
                                                                                                                                                                                                                             WO9818930-A2
                                                                                                                                                                                                                                                                              detection; pneumonia; otitis media; meningitis.
                                                                                                                                                                                                                                                                                                                                             02-OCT-1998
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k----avedakakildgsvkvpekz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stlkqvgttvkdi-----snkaergefpggq---vivyslkdkgvdlavtnlseegk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            esevisrfeagfkagv----asvdpsikvqvdyag-sfg-daakgktiaaaqyaagad-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSTLLAVAGPL-TEIFSDIIANQNDR-----YLIGVDTDQSL--VYT----KTKNKFFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDK
                                                                                                                          HUMAN GENOME SCI INC
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25.5%;
                                                                                                 Johnson
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Pred. No. 2.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, office media or meningitis. Probes based on the nucleic acid
04-MAY-1998;
                                                                                               Enterococcus
                                                                                                                                                                              Enterococcus
                                                                                                                                                                                                                                               AAY00049;
                                                                                                                                                                                                                                                                             AAY00049 standard;
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                                12-NOV-1998
                                                                WO9850554-A2
                                                                                                                                detection;
                                                                                                                                             Enterococcus faecalis; infection; vaccine;
                                                                                                                                                                                                              20-APR-1999
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                                                                                                                                attenuation;
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                                                                                                                                                                            faecalis antigenic polypeptide fragment EF021.
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98WO-US08959
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25.7%;
                                                                                                                              antigenic
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Pred. No. 5.4e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -gfalnna-----vkdaakehtdlnyv
                                                                                                                                             immune response; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 328;
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AAW61758
ID AAW6
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AC AAW6
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AAW61758 st; AAW61758; 09-SEP-1998

(first entry)

RESULT 11

standard;

Protein;

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Best Local
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
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                             354 VDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD 403
                                                                                                                 197 kgkalaaamyqngvdiifhasgatgqgvfqeakdlnesgsgdkvwvigvdrdqdadgky-
                                                                                                                                                  262 TLLAVAGPLTEIFSDII----
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                                                                                                                                                                                                                                                                                                                                                                                         33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGE----
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vdltdgyl--ndkt----
                                                                                                                                                                                                                                                          ktkdgkednftltstlkgvgtavqdianraledk-
                                                                                       KTK-----NKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF
                                                                                                                                                                                vvidrfqagfekgv-adaakelgkeitvdt------kyaasfadpa
                                                                                                                                                                                                                                        ddqidgkknv-----vsatfrdneaaylagvaaa-----
                                                                                                                                                                                                                                                                                                                             ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0066009.
97US-0044031.
97US-0046655.
                                                                                                                                                                                                                                                                                                                                                                                                                                   8.3%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hromockyj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
-----keavktakdkvisgdvkvpekpe
                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 178; DB 20;
Pred. No. 4.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۶
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                ----ANQNDR-YLIGVDTDQSL--VYT
                                                                                                                                                                                                                                      --netktnkvgfvggeeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 339;
                                                        fpggehlvy-glkdgg
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to develop vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                298
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В.

burgdorferi antigenic protein

p39 beta.

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Best I
                                                                                                                                                                                                                                                                                                                               tches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-1991;
05-MAR-1990;
19-FEB-1993;
01-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                             This represents the Borrelia burgdorferi antigenic protein p39 beta. The antigenic protein p39 alpha is immunoreactive with mammalian Lyme borrelios serum. The Borrelia antigenic proteins p39 alpha and p39 beta are used in vaccines to protect against Lyme disease, as assay reagents to detect specific antibodles in the serum (diagnostic of Lyme disease), and to raise antibodles, either for diagnosis (by detecting the corresponding antigen) or in screening agents for ability to inhibit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antigenic for raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schwan TG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1995;
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 385
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                          278
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                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                        Match
                                                                                                                                                                                                                                                                                                    ANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSSTAELEGKYSS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-413001/35
DB; AAV35685, AJ
                                                                                                                                                                                                                                                                           sskkikismlv---dgvlddksfnssaneallrlkkdfpenieevfs--caisgvyssyv
                                                                                                                                                  AGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASK--DKPSTLLAV
                                                                                                                                                                                                                                                    --LANTNKN----VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI 153
KTIPAEEVRKTLEIP
                      iknnnv-----weggk----vvqmglrdgviglpnan
                                                TKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKT 384
                                                                         aaglagigvieaaknigdgyyvigadqdqs--ylapkn-fitsviknigdalylitge-y
                                                                                                AGPLTEI-FSDIIANQND-RYLIGVDTDQSLYYTKTKNKFFTSILKNLGYSVFSVLSDLY
                                                                                                                        ygyesgakyan-kdieilseysnsfsdvdig-----rtiasknyskgidvihf
                                                                                                                                                                           a-----igfiggmkgnivdafr
                                                                                                                                                                                        PTGRYINLTYKTEEAGWLAGY--ANASFLAKKFPSDPTKRSAIVIG--GGISPAVTD-FI 208
                                                                                                                                                                                                                            sdldnlkrngsdliw-lvgymltda--sllvssenpki--sygiidpiygddvqipenli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           borreliosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Columns 31-34;
                                                                                                                                                                                                                                                                                                                                                                                                                    of the
                                                                                                                                                                                                                                                                                                                                                                                             341 AA
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simpson WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins from antibodies or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90US-0487716.
93US-0020245.
95US-0396957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-0664731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyme
                                                                                                                                                                                                                                                                                                                                                                                                                   proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV35687
                                                                                                                                                                                                                                                                                                                                         8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigenic protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33pp;
                                                                                                                                                                                                                                                                                                                               58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borrelia burgdorferi useful for diagnostic detection of
                                                                                                                                                                                                                                                                                                                             Score 178; DB 19;
Pred. No. 4.8e-06;
8; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha;
                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p39
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                        ef-eyi
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                                                                                                                                                                                                                                                                                                                                                                                                                               detecting
ty to inhibit
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RESULT 1
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Best Local Similarity
Matches 103; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a protein isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening compounds to identify agonists and antagonists of E. faecalis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 100; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bailey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-NOV-1997;
06-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY00048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-1997;
                              203
                                                                                  135
                                                                                                                                   143
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AVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPS
                                                                                                                                                                                                                                                                                                                                                 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA----LTGGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-070095/06
                                                                                                        GIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP:||: ||: || : ||
                                                                            ddq1dgkknv-----vsatfrdneaaylagvaaa-----netktnkvgfvggeeg
                                                                                                                                                                                                                                                                                           ktaesgggkgda----ahsaviitdtggvddksfnqssweglqawgkehdlpegskgyay
                                                                                                                                                                                     iqsndaadyttnidqavsskfntifgi----gyllkda-----issaadanpdtnfvli 134
                                                                                                                                                                                                                                      ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            faecalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           faecalis protein
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97US-0044031.
97US-0046655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GH,
                                                                                                                                                                                                                                                                                                                                                                                                                            8.3%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hromockyj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigenic
                                                                                                                                                                                                                                                                                                                                                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                   Score 178; DB 20;
Pred. No. 5.3e-06;
1; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EF021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      develop
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 1
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                interleukin-X (IL-X), from an Epstein Barr virus (EBV)-carrying lymphoblastoid cell line. IL-X proteins can be used to enhance the growth of cells in vitro, or to grow primary human B cell cultures to facilitate proliferation of these cell lines, as therapeutics or prophylactics, as molecular weight standards, as inert proteins in an assay, or in the detection of antibodies that are immunoreactive with IL-X. Nucleotide sequences encoding the peptides could be used to produce recombinant peptides or they could be used as probes or primers for diagnostic and/or analytical polymerase chain reaction (PCR) procedures, or as DNA or RNA sizing standards. The present sequence represents the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2001
                                                                                                                                                       The invention relates to a novel secreted autostimulatory factor, interleukin-X (IL-X), from an Epstein Barr virus (EBV)-carrying
                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                                                      Blazar BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2001019713-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JAN-2002
          sequence of IL-X.
                                                                                                                                                                                                                               New II-x polypeptides useful e.g. for enhancing the growth of cells vitro, for growing primary human B cell cultures to facilitate proliferation of these cell lines, as therapeutics or prophylactics, molecular weight standards -
                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-1994;
11-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JAN-2001; 2001US-0760541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU07352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU07352 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                   (BLAZ/) BLAZAR B A.
(WEBB/) WEBB A C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interleukin-X;
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                                                                                                                                                                                                   Page 7; 16pp;
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   B cell.
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Best Local
            proteins was isolated by polymerase chain reaction (PCR) using the primer sequences given in AAQ34673-76. This DNA contained two open reading frames (ORF). It was therefore concluded that the P39 antigen which has been previously described is not one protein but two, 39-alpha and 39-beta. The P39 signal appears to be enhanced when both genes are present. Gene 1 encodes a 339 amino acid protein with a calculated molecular weight of 36.926 kD. The protein encoded by this gene which is reactive with serum from human Lyme patients. The ORF
                                                                                                                                                                                       New Borrelia burgdorferi protein and DNA isolates -detection of Lyme borreliosis infection and in production and vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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of gene
                                                                                                                      The sequences given in AAR31013 and AAR33280 represent the B. burgdorferi proteins P39-alpha and P39-beta. The DNA encoding these
                                                                                                                                                                 Disclosure;
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11-MAY-1993
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                                                                                                                                                                                                                                                                                       Simpson
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  been designated p39-beta.
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bred. No. 4.2e-06;
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ribosomal binding site; F
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleotides downstream of p39-alpha and encodes a protein of 341 amino acids (37.506 kD). The promoter located 5′ of p39-alpha appears to be present with classic -10 and -35 regions whereas p39-beta lacks a recognisable promoter sequence. Both genes have putative ribosomal binding sites immediatly 5′ to the start codons and each is terminated with a TAA codon. Comparing the gene sequences of p39-alpha and p39-beta indicates that these genes have 62% similarity. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                                                                                                                                                                               Polymerase chain reaction; PCR; primer; open reading frame; ORF; P39, antigen; 39-alpha; 39-beta; serum; human; Lyme patient; p39-beta; p39-alpha; promoter; -10; -35; ribosomal binding site; RBS.
                 05-MAR-1990;
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                                                                                01-DEC-1992
                                                                                                                                                Borrelia burgdorferi
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11-MAY-1993
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                 90US-0487716
                                                90US-0487716.
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Pred. No. 1.8e-05;
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Schwan TG, Simpson WJ;

XX

Schwan TG, Simpson WJ;

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WPI; 1993-017799/02.

DR N-PSDB; AAQ34672.

XX

New Borrelia burgdorferi protein and DNA isolates - used in detection of Lyme borreliosis infection and in prodn. of PT antibodies and vaccines

PT New Borrelia burgdorferi protein and DNA isolates - used in detection of Lyme borreliosis infection and in prodn. of PT antibodies and vaccines

PT New Borrelia burgdorferi proteins and prodn. of PT antibodies and vaccines

NX

Disclosure; Page 36-39; 69pp; English.

CC proteins was isolated by polymerase chain reaction (PCR) using the proteins was isolated by polymerase chain reaction (PCR) using the proteins was isolated by polymerase chain reaction (PCR) using the protein base been previously described is not NA contained two open cadding frames (ORF). It was therefore concluded that the P39 antigen which has been previously described is not no protein but two, 39-alpha and 39-beta. The P39 signal appears to be enhanced when both genes and 39-beta. The protein encoded by this calculated molecular weight of 36,926 kD. The protein encoded by this calculated molecular weight of 36,926 kD. The protein encoded by this calculated in the Calculated page of P39-alpha and encodes a protein of 341 amino acid gene 2 has been designated p39-beta. This genes ORF starts 116 calculated (37.506 kD). The promoter located 5' of p39-alpha appears to be present with classic -10 and -35 regions whereas p39-beta lacks a recognisable promoter sequence. Both genes have pate the pate and p39-alpha patend number. For further information please visit hongoing US granted patent numbers. For further information please visit the Derwent calculated by site at www.derwent.com/dwpi/updates/ntis_us.html.)

Sq Sequence 340 AA;
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Query Match
Best Local Similarity 22.7 406 286 346 239 286 189 232 143 173 114 93 37 PDKQQESLDKLITD YLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQ 405 LIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATV 345 DKI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQ--NDRY gyiaakl-----sktgkigflggiegeivdafrygyeagakyan----kdikist GYANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITT GFQHGD-AFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLA 172 gtfddksfnesalngvkkvkeefkielvlkesssnsylsdleg----lkdagsdliwlig 92 GTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYSSLANTNKN-VWVLS 113 nyglkegvvgfv-iigvdedqayl---apdnvitsttkdvgral----nift--snhlktntfeggk---li qyigsfadleagrsvatrmysdeid-----iihhaaglggigaievakelgsghy fyrfsdvakvaalqnpdmkyai-----idpiysndpip-anlvgmtfraeegaflt 142 7.68; 22.78; 69; Score 164.5; DB 1 Pred. No. 5.8e-05; 59; Mismatches 135 DB 14; 135; Indels Length 340; 85; Gaps 285 238 285 188 231 326 19;

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DB seq length: 0
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2155
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1253.726 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
                                                                                           283138 seqs, 96089334 residues
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Database PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* pir1:*
pir2:*
pir3:*

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. score grea and is der No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	5	σı	4	ω	2	1	No.	Result
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ALIGNMENTS

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ABC transporter xylose-binding lipoprotein [imported] - Mycoplasma pulmonis (strain U C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: B90555
R;Chambaud, I:; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: B90555
A;Status: preliminary
A;Accession: preliminary
A;Residues: 1-461 <KUR>
A;Cross-references: GB:AL445566; PID:g14089760; PIDN:CAC13519.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP RESULT B90555

C;Genetics: A;Gene: MYPU_3460 A;Genetic code: SGC3

Db Qy Db	Oy Oy	Oy Oy Db	Que Bes Mat Oy
322 334 382	167 EAGWLAGYANASFLAKKFPSDPTKRSAI	62 NDNSFNQSGWEAIQQLGALTGGEITS	Query Match Best Local Similarity 31.2%; Pred. No. 5.1e-27; Matches 133; Conservative 82; Mismatches 161; Indels 50; Gaps Oy 13 ADNQNKQITDVSKISGLYNERKSEIMAAKADANKHFGLNMAIVTAGGTV 61
ALLTKDEESVILKEGNDKFL 381 SEAKKEFEEKTKTIPAEE 391 :	VIGGGISPAVTDFIAGYLAGIKAWNLKNSD 224	VDSSTAELEGKYSSLANTIK 107 :: :	; Length 461; 7; 61; Indels 50; Gaps 11; ADANKHFGLNMAIVTAGGTV 61 : ::: : LETQKVVLITADGNI 82

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C;Species: Streptococus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: G95097
R;Tettelin, H; Nelson, K.E; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heison, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, on, J.D.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
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9:Idues: 1-350 <STO>
A;Cross-references: GB:AE005176; PID:g12724428;
A;Experimental source: strain IL1403
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                   TSLEGNDKKLATEAISEAKKEFEEKTKTIPAE 390
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A;Gene:
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J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5718, 2001
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A;Molecule type: DNA
A;Molecule type: CNA
A;Residues: 1-350 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK74976.1; PID:gl4972319; GSPDB:GN00164; TIGR:
A;Experimental source: strain TIGR4
C;Genetics:
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A; Residues: 1-374 < KUR>
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C;Accession: C97965
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                              RKSEIMAAKADANKHFĞLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGEITSVD
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RSSRNAASSSDVK----TKAAIVTDTGGVDDKSFDQSAWEGLQAWGKEHNLSKDNGFTYF 104
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                                                                                                                                                                                                                                                                                                                                                             GB:AE007317; PIDN:AAK99551.1; PID:g15458340; GSPDB:GN00174
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25.7%;
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                                                                                                                                                           Score 198; DB 2;
Pred. No. 4.6e-05;
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Pred. No. 2.4e-05;
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                                                                                                                                                                                          Length 374;
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GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNII 140

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probable lipoprotein, Med/BMP family [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C;Accession: D96986 R;Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bennett, G.N.; Koonin, E.V.; Smith, D.R. A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: D96986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001437; PIDN:AAK78679.1; A;Experimental source: Clostridium acetobutylicum C;Genetics: A;Genee: CAC0702
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A; Molecule type: DNA
A; Residues: 1-357 <KUR>
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  VILTSMVKRVDIATYNTVKDLVKGKK-----
                                           KFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLG: KDRFVDIADTSLE 362
                                                                                                                                                                                                                                                                                                          E-----KNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDP
                                                                                        GKEVATSLYNGGCDIVYHAAGGAGIGVF-DVAKSLRDQGKDVWAIGVDKDQAAGLPKYAD
                                                                                                                               -KERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQNDR----YLIGVDTDQSLVYTKTKN
                                                                                                                                                                             TKTNKIGFVGGKDQPLINKFLSGYIAGAKTVN----PNITVEK---NYTNDYSDTSK
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Pred. No. 0.0001
7; Mismatches 1
                                                                                                                                                                                                                                                               --MSLVFKEQEGSFLMG----VIAGKM----
  FEGGKVES - - - FGLKEDGVGVAPTS - -
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A.Gene: tmpC; TP0319
A.Start codon: GTG
G.Superfamily: ABC transporter yufN
C.Superfamily: ABC transporter yufN
C.Keywords: blocked amino end; lipoprotein; membrane protein; thiolester bon
F.1-20/Domain: signal sequence #status predicted <SIG>
F.21-353/Product: membrane lipoprotein tmpC #status predicted <MAT>
F.21/Modified site: fatty acylated amino end (Cys) (in mature form) #status
F.21/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-10, 'A', 12-158, 'R', 160-353 <SCH>
A; Residues: GB: X57836; NID: 48838; PIDN: CAA40968.1;
A; Note: this protein is shown to incorporate palmitic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Schouls, L.M.; van der Heide, H.G.J.; van Eml
Infect. Immun. 59, 3536-3546, 1991
A;Title: Characterization of the 35-kilodalton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Complete genome sequence of Treponema pallidum, the syphilis A;Reference number: A71250; MUID:98332770 A;Accession: H71340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane lipoprotein TmpC precursor - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 07-Aug-1998 #sequence_revision 07-Aug-1998 #text_change 23-Jul-1999
C;Accession: H71340; A43595; S29561
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A; Accession: A43595
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Best Local S
Matches 86
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  EIP
                                                                                                                                                                                                                                                                                                                                                     LAGYANASFLAKKFPSDPTKRSAI--VIGG--GISPAVTDFIAGYLAGIKAWNLKNSDKK 226
                                                                                                                                                        ANQNDRYLIGVDTDQSL--VYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGF
                                                                                                                                                                                                                                                                                                                                                                                                 VACGSFLVEA-----VIETSARFPKQKFLVIDAVVQDRDNV-----VSAVFGQNEGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                     VLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGW
                                                                                                                                                                                                                      -----PDIQVVVEVANTFSDPQKGQALAAKLYDSGVNVIFQVAGGTGNGVIKEARDRR
                                                                                                                                                                                                                                                               TKITTDKIEINLGFDVQDT-STKERLEQIASK---DKPSTLLAVAG----PLTEIFSDII
                                                                                                                                                                                                                                                                                                          LVGVA-AALKAKE-----AGKSAVGFIVGMELGMMPL---FEAGFEAGVKAVD-----
                                           ----GQSIMFGLEDKAVGIPE----
                                                                                      EFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.4%; Score 181; DB 1;
23.7%; Pred. No. 0.00049;
1tive 69; Mismatches 134
                                             -ENPNLSSAVMEKIRSFEEKI---
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PID: 9332

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A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Hennut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle ger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, thors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serora Keuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K., Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.; Reference number: A69580; MUID:98044033
A.; Accession: C70009
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A; Residues: 1-350 <KUN>
A; Cross-references: GB:Z99120; GB:AL009126;
A; Experimental source: strain 168
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Best Local
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                                                                                                                                                                                                                                                                                                              UDVIYHSAGATGTGVETE-AKNLKKEDPKRDVWVIGVDKDQYAEGQVEGTDDNVTLTSMV
                                                                                                                                    -KAVDKWKKKIIDGLEIPATEKELKTFKAE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                              PAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDT--STKERLEQIASKDK 259
                                                                                                                                                                                                                         K----KVDTVVEDV-TKKASDGKFPGGE-----TLTYGLDQDGVGISPSKQNLSDDVI-
                                                                                                                                                                                                                                                                                                                                                                                                     ELIKKFEVGFRAGVQAVNPK-----AVVEVKYAGGFDKADVGKATAESM----YKSG
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                                                                                                                                                                                                                                                                  KNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLA 369
                                                                                                                                                                                                                                                                                                                                                          PSTLLAVAGPL-TEIFSDIIAN-----QNDRYLIGVDTDQ---SLVYTKTKNKFFTSIL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDAVVDKDNV-----ASITEKEQEGSELVGVAAAL-----SSKSGKIGEVGGMES
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25.9%;
                      Thermotoga
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Pred. No. 0.00052;
0; Mismatches 144;
                      maritima
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                         (strain MSB8)
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basic membrane lipoprotein B (bmpB) - Lyme disease spirochete
;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Date: l3-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999
C;Accession: E70147; I40290; I40242
R;Fraser, C.M.; Casjens, S.; Huang, M.M.; Sutton, G.G.; Clayton, R.; Lathigra, Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hat Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A/2200; MUID:99287316
A; Accession: F72418
A; Status: preliminary
A; Molecular transport
A;Cross-references: GB:AE001143; A;Experimental source: strain B31 R;Simpson, W.J.; Cieplak, W.
                                                                                                                               Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943
A;Accession: E70147
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; RiC.M.
                                                                 A; Molecule type: DNA
A; Residues: 1-341 < KLE>
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C; Superfamily:
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                                                                                                           A;Status: preliminary; nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGIS-PAVTDFIA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISE---AKKEFEEKTKTIP-AEEVRKTLEIPEM 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEAAREKFSA-LAGSDKLVDLIDYYTTNGKGFFAIGVDMDQDYM---APGAVLTSAMKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- ASKDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYEAGIKTYSVLHK-KNVKILRGYTQDFEDPKKGKDLAMSQFAEGADIVFHASGACGNGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTE- 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDS-S 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSDYIPNLSKAAEEADLVFAVGFMMTNDLFKVAKQYPDT-----YFVGIDITPPEG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKFLVISLMIFAVALFGFKVIMVTDVGGLGDKSFNDGTWAGIKQAAEELGIEAKVIQSYE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-359 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GTFEGGHR----VLGISEDAVGI--SPMKYTKGLVPNRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 178.5; DB 2;
; Pred. No. 0.00071;
59; Mismatches 177;
                                               GB:AE000783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB:AE000512; NID:g4980582; PIDN:AAD35196.1; PID:g498
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                                                                                                             not shown;
                                            NID: g2688279;
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                                                                                                                                                                          Borrelia
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                                               PIDN: AAC66758.1;
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                                                                                                                                                                                                                                           on, M.;
Hatch,
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D.; Jones, L.M., N. 2001
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J. A; Title: Comparative genomics of Listeria species.
A; Title: Comparative AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Nucloetide sequence and analysis of the gene in Borrelia burg A;Reference number: I40289; MUID:94327086
A;Recession: I40290
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: I-232,'A',234-317,'V',319-341 <RES>
A;Cross references: GB:L24194; NID:9508420; PIDN:AAA72407.1; PID:g5084
R;Ojaimi, C.; Davidson, B.E.; Saint Girons, I.; Old, I.G.
Microbiology 140, 2931-2940, 1994
A;Title: Conservation of gene arrangement and an unusual organization A;Reference number: I40241; MUID:9511614
A;Accession: I40242
                                                      A;Reference number: AB1077;
A;Accession: AB1610
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GLA>
                                                                                                                                                                                                                                                CD4+ T cell-stimulating antigen, lipoprotein [imported] · Listeria innocua (strain C;Species: Listeria innocua (c;Species: Listeria innocua (c;Species: Listeria innocua (c;Species: C;Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 C;Accession: AH1610 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsih
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A;Molecule type: DNA
A;residues: 1-44,'A',46-179 <RE2>
A;Cross-references: GB:L35050; NII
A;Cross-references: GB:AL592022; PIDN:CAC96656.1; A;Experimental source: strain Clip11262 C;Genetics:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LANTNKN----VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTGRYINLTYKTEEAGWLAGY - - ANASFLAKKFPSDPTKRSAIVIG - - GGISPAVTD - FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSKKIKISMLV---DGVLDDKSFNSSANEALLRLKKDFPENIEEVFS--CAISGVYSSYV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKNNNV-----WEGGK----VVQMGLRDGVIGLPNAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGPLTEI-FSDIIANQND-RYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASK--DKPSTLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A-----VVFRVEQGAFLAGYIAAKKSFSGK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDLDNLKRNGSDLIW-LVGYMLTDA--SLLVSSENPKI--SYGIIDPIYGDDVQIPENLI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTIPAEEVRKTLEIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATI:AISEAKKEFEEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGLAGIGVIETAKNLGDGYYVIGADODOS--YLAPKN-FITSVIKNIGDALYLITGE-Y
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protein C
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Pred. No. 0.00082;
9; Mismatches 124
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                                        PID:g16413898; GSPDB:GN00178
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                                                                                                                                                                         Maitournam, A.; Ma
Voss, H.; Wehland
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Fsihi, H.
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Matches 101;
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Best Local :
                                                                                                                                                                          206 ANDFAKADKGQQIASSMYSSGVDVIFHAAGGTGNGVFAE-AKNLKKKDPSRAVWVIGVDR
                                                                                                                                                                                                                                                                     164
                                                                                                                                                                                                                                                                                                                                                              124
313 IEYGLDKDAVGLSE-----HQDNISKDVLAKVE---EYKQKIVDGD-----IKVPEKP
                                     345 VYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMP
                                                                                                                                                                                                                                                                                                                 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 SGLV-----NERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                         QKPKNQFAIVDDTI-----DDRDNVVSIG-----FKDNDGSYLVGVVAGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGVVLGACGSSSDDKKS-----GDDKSSKDFTVAMVTDTGGVDDRSFNQSAWEGLQKFG
                                                                                                                  DQ-----SLYYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSAT
                                                                                                                                                                                                                         --DTSTKERLEQIASKDKPS----TLLAVAGPLTEIFSDIIANQNDR-----YLIGVDT
                                                                                                                                                                                                                                                                     --TTKTNKVGFVGGVKGAVIDRFEAGFTAGVKA-------VNPNAQIDVQY
                                                                                                                                                                                                                                                                                                               SDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KANDMEKGTDGYNYLQSASEADYK-----TNLNTAVRSDYDLIYGIGYKLKDAIEEVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALT----GGEITSVDSSTAELEGKYSSLANTNKNVWVLS------GFQHGDAFTRWLK 126
                                                                                      DQWDEGKVTANDGKDYNVTLTSEIKRVDIAV----DDLAT-----RTKAGDFPGGTK---
                                                                                                                                                                                                                                                                                                                                                                                                        - IPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 173; DB 2; Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
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357
                                                                                                                                                                            264
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A; Molecule type: DNA
A; Residues: 1-516 <GLA>
A; Cross-references: GB: AED002100; CA; Experimental source: serovar 3; hypothetical protein UU012 [imported] - Ureaplasma C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 A; Gene: UU012 A; Genetic code: A;Description: The complete sequence A;Reference number: A82870 A;Accession: C82946 C;Accession: C82946
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, A; Status: preliminary submitted to GenBank, February 2000 Query Match Best Local S Matches 110 Genetics: 157 --RYINLTYKTEEAGWLAGYANASFLAKK---FPSDPTKRSAIVIGG--GISPA-VTDFI Local Similarity hes 110; Conserv 17 48 FGLNMAIVTAGGTVNDNSFNQSG--WEAIQQLGALTGGEITSVDSSTAE-LEGKYSSLAN 104 11 TNKNVWVLSGFQHGDAFTRWLKIPENKQ -- LFTEK -- - NIIIL -- - GIDWTDTENVIPTG FALGTITVATSCTQKSTLNYSQFYW-----TSPTSDDDEGFQTKYKSMAS ADRVADVYFKVDEAAFLGGIAAAYMLNSNQAVFGAD---SGC3 Conservative 7.8%; 25.1%; GB:AF222894; NID:g6898946; PIDN:AAF30417.1; ; biovar 1 PERLQNALVNDKFDPNLIALILDGVYNNDNKAEFYKG Score 168.5; DB 2; Pred. No. 0.0051; 5; Mismatches 167; of Ureaplasma 20-Aug-2000 #text_change NKLTWGGYVGINAKNTTNYL urealyticum: urealyticum Length Indels 516; Alternate views 20-Aug-2000 E.Y.; Cassell, Gaps 156 168 112 62 26; GSPDB:GN G.H.

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A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Sinces, N.; Tierrez, A.; Vazquez-Boland, J. A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Recession: AD1248
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; )
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AD1248
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A; Residues: 1-357 < GLA>
A; Residues: 1-357 < GLA>
A; Cross-references: GB:NC_003210;
A; Experimental source: strain EGD-
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tches 98
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                  272
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               VTANDGKDYNVTLTSEIKRVDIAV----EDLAT----RAKAGDFPGGTK---IEYGLDK
                                               -SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSATVYLGIKD
                                                                                DKGQQIASSMYSSGVDVIFHAAGGTGNGVFAE-AKNLKKKDPSRAVWVIGVDRDQWDEGK
                                                                                                             ERLEQIASKDKPS----TLLAVAGPLTEIFSDIIANQNDR-----YLIGYDTDQ-----
                                                                                                                                                  KVGFVGGVKGTVIDRFEAGFTAGVKA----
                                                                                                                                                                               AIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQ----DTSTK
                                                                                                                                                                                                                AIVDDTI-----DDRDNVVSIG-----FKDNDGSYLVGVVAGL-----TTKTN
                                                                                                                                                                                                                                              LFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRS
                                                                                                                                                                                                                                                                               GTDGYNYLQSASEADYK-----TNLNTAVRSDYDLIYGIGYKLKDAIEEVSKQKPKNQF 130
                                                                                                                                                                                                                                                                                                              GGEITSVDSSTAELEGKYSSLANTNKNVWVLS-----GFQHGDAFTRWLK-IPENKQ
                                                                                                                                                                                                                                                                                                                                              ILGACGSSSDDKKSSDDKSSKDF--TVAMVTDTGGVDDRSFNQSAWEGLQKFGKANDMEK
                                                                                                                                                                                                                                                                                                                                                                              ISGLVNERKSEIMAAKADANKHEGLNMAIVTAGGTVNDNSENQSGWEAIQQLGALT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASKDKPSTLLAVAGPLTEI-FSDIIANQNDRY-LIGVD----TDQSLVYTKTKNKFFTSI
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                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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23.8%;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 357;
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Fsihi, H.
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                                                                                            A; Description: The complete A; Reference number: A82870 A; Accession: C82914
                                                                                                                                                                                                                                              RESULT
C82914
A; Experimental source: C; Genetics:
                                              A; Molecule type: DNA
A; Residues: 1-525 <GLA>
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A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete,
A;Reference number: A70100; MUID:98065943
A;Accession: H70147
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A; Residues: 1-360 < KLE>
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                                                                              A; Status: preliminary
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Best Local Similarity
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A;Cross-references: GB:AE002123; GB:AF222894; NID:g6899229; PIDN:AAF30635.1; A;Experimental source: serovar 3; blovar 1
                                                                                                                                                                                                                                                                 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, submitted to GenBank, February 2000
                                                                                                                                                                                                                                                                                                                                conserved hypothetical membrane lipoprotein UU226 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: C82914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKYAN-----SNIKVVSQYVGTFGDFGLG-----RSTASNM----YRDGVDIIFAAAG-L 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VACSSSDDGKSEAKTVSLI-VDGAFDDKGFNESSSKAIRKLKADLNINIIEKASTGNSYL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSSTAELE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -NLLNISFRSEEVAFLAGY------FASKASKTGKIGFVGGVRGKVLESFMYGYEAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKYSSLANTNKN-VWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGIGVIEAAKELGPDHYIIGVDQDQSYL---APNNVIVSAVKKVDSLMYSL---
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                                                                                                                                                                                                                                  sequence of Ureaplasma urealyticum:
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                                                                                                                                                                                                                                     Alternate views
                                                                                                                                                                                                                                                                                                    E.Y.; Cassell,
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basic membrane protein A (bmpA) - Lyme disease spirochet:
N;Alternate names: antigen P39; membrane lipoprotein A
C;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999
C;Accession: F70147; 140289; 140241
R;Fraser; C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.;
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.;
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-339 <RES>
A.F. Cross references: GB:L24194; NID:g508420; PIDN:AAA72406.1;
A.Cross references: GB:L24194; NID:g508420; PIDN:AAA72406.1;
R.Ojaimi, C.; Davidson, B.E.; Saint Girons, I.; Old, I.G.
Microbiology 140, 2931-2940, 1994
A.Title: Conservation of gene arrangement and an unusual orga
A.F. Title: Conservation of gene arrangement and a.Reference number: I40241; MUID:95111614
A.Recession: I40241
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                        FEMS Microbiol. Lett. 119, 381-388, 1994
A; Title: Nucloetide sequence and analysis of the A; Reference number: 140289; MUID:94327086
                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-339 <KLE>
A; Cross-references: GB: AE0001143; GB: AE000783;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
bforence number: A70100; MUID:98065943
Accession: F70147
A; Status: preliminary; nucleic acid sequence not shown; "ranslation not shown
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A;Genetic code:
                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain B31 R; Simpson, W.J.; Cieplak, W.
                                                                                                                                                                                                                                  A; Accession: I40289
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illarity 22.9%;
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A;Cross-references: GB:L35050; NID:g516591; PIDN:AAC41401.1; PID:g516592
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                                                                                                                                                               IGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVY 346
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Search completed: July 18, 2002, 15:29:56 Job time: 43 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
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UTSA_LISIN
BMFB_BORGA
TCSA_LISMO
BMFB_BORGA
TCSA_LISMO
BMFA_BORBU
BMFA_BORBU
BMFA_BORBU
BMFA_BORBU
BMFA_SORBU
BMFA_STAAU
PEDA_STRAY
Y040_MYCGE
BMFC_BORBU
YC40_MYCFN
YC40_MYCFN
YC40_MYCFN
YC40_MYCFN
YC40_MYCFN
YC47_SCHPO
XCFC_XENIA
YA47_SCHPO
XCFC_XENIA
PARC_BORBU
TBFL_WEAST
YA47_SCHPO
XCFC_XENIA
FLGK_SALTY
SCA4_RICAK
FLAME
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FLGK_SALTY
SCA4_RICAK
FLAME
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YA42_MYCCN
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P506379
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045011
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031362
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0447286
050168
050663
99351
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 5 mycoplasma
8 mycoplasma
9 schizosacch
2 xenopus lae
6 borrelia bu
9 neisseria m
2 salmonella
9 rickettsia
9 rickettsia
9 rickettsia
9 shigella fil2 saccharomyc
8 flavobacter
1 streptococc
2 mycoplasma
0 streptococc
9 escherichia
                                                                                                                                                                                                                                                                 7 borrelia ga
4 treponema p
2 bacillus su
1 borrelia bu
1 listeria in
2 borrelia af
2 borrelia af
3 borrelia bu
0 borrelia bu
0 borrelia bu
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2 borrelia bu
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3 staphylococ
2 mycoplasma
9 rickettsia
6 escherichia
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Result No.

Score

181
180.5
173
169
168
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165.6
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152.5
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PLC_LISMO	YNI7_YEAST	SLAP_BACSH	RPOB_ASTLO	HTPG_BUCAI	YN8H_YEAST	RPO1_FOWPV	ECE1_HUMAN	ANT1_ONCVO	YC84_MYCPN	BRC2_HUMAN	LBPA_NEIMA
P34024	P48231	P38537	P27059	P57555	P53729	Q9j593	P42892	P21249	P75493 I	PS1587	Q9jtk4
list	sacc	baci	astas	buchn	sacch	fowlpo	homo :	onchoo	mycoplasma	homo ;	neisse

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Title: Perfect score: Sequence:

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Matches 93
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STRAIN-TICHOLS;
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STRAIN-TICHOLS;
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Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Praser C.M., Norris S.J., Weinstock G.M., Wetchum K.A.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Dodson R., Gwinn M., McLeod M.P., Salzberg S., Peterson J.
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.
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Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.
Sodergren E.
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P29724; 083339;
01-APR-1993 (Rel. 25, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updathementrane lipoprotein tmpC precursor (Membra
                                                                               Venter J.C.;
"Complete genome sequence spirochete.";
Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                Schouls L.M., van der Heide H.G.J., van Embden J.D "Characterization of the 35-kilodalton Treponema pallidum recombinant lipoprotein TmpC and antibody lipidated and nonlipidated T. pallidum antigens,"; infect. Immun. 59:3536-3546(1991).
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-NICHOLS; MEDLINE-91372962;
     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treponema pallidum.
Bacteria; Spirochaetales;
                               -1- SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                   SUBCELLULAR
                                                   (Probable)
     SWISS-PROT
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93; Conser
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                                                                   LOCATION:
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der Heide H.G.J.,
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                                                                                                                Treponema
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Pred. No. 0.
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                                                                                                                  pallidum,
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mith H.O.,
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   collaboration
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   RESULT
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                                                                                                                                                                 LBACSU
YUFN_BACSU
005252;
               Bacillus subtilis.
Bacteria; Firmicutes; Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID-1423;
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15-DEC-1998

(Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 40, Last annotation update)
1 lipoprotein yufN precursor

update)

update)

Bacillus/Clostridium

group;

STANDARD;

PRT;

350

B

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Query Match
Best Local
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CONFLICT
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SIGNAL
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the Euro
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LIPID
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EMBL; AE001211; AAC65302.1; -.
PIR; A43595; A43595.
PIR; S29561; S29561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
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343
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European Bioinformatics Institute. There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                      MAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST-AELEGKYSSLANTNKNVW 110
ΨV
                                                            -----GQSIMFGLEDKAVGIPE-----ENPNLSSAVMEKIRSFEEKI--
                                                                                                                                                                                                                                                                             LAGYANASFLAKKFPSDPTKRSAI -- VIGG -- GISPAVTDFIAGYLAGIKAWNLKNSDKK
                                                                                                                                                                                                                                                                                                                                           VLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGW 170
                                                                                        EFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTL
                                                                                                                        LNGQDVWVIGVDRDQYMDGVYDGSKSVVLTSMVKRA-----DVAAERISKMAYDGSFPG-
                                                                                                                                                      ANONDRYLIGVDTDQSL--VYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGF
                                                                                                                                                                                                               TKITTDKIEINLGFDVQDT-STKERLEQIASK---DKPSTLLAVAG----PLTEIFSDII 278
                                                                                                                                                                                                                                                                                                              VACGSFLVEA-----VIETSARFPKQKFLVIDAVVQDRDNV-----VSAVFGQNEGSF
                                                                                                                                                                                                                                                 LVGVA-AALKAKE-----AGKSAVGFIVGMELGMMPL---FEAGFEAGVKAVD------
                                                                                                                                                                                                                                                                                                                                                                                                                                     86;
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CLEAVAGE AT ALTERNATIVE PROCESSING SIT
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                          BMPB_BORBU STANDARD; PRT; 341 AA Q45011; 007954; 031317; 050168; Q44858; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ptam; PF02608; Bmp; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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Ojaimi C., Davidson B.E., Saint-Girons I., Old I.G., "Conservation of gene arrangement and an unusual organization genes in the linear chromosomes of the Lyme disease spirochaet Borrella burgdorferi, B. garinii and B. afzelii.", Microbiology 140:2931-2940(1994).

-i- SUBCELLULAR LOCATION: Attached to the membrane by a lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjons S., Huang W.M., Sutton G.G., Clayton Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman Utterback T., Watthey L., McDonald L., Artiach P., Bowman Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Smith H.O., Venter J.C.;
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Simpson W.J., Cieplak W., Schrumpf M.E.,
"Nucleotide sequence and analysis of the
encoding the immunogenic P39 antigen.";
FEMS Microbiol. Lett. 119:381-388(1994).
                                                                                                                   EMBL;
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EMBL;
                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement.
                                                TIGR; BB03
InterPro;
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[5]
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"Heterogeneity of BmpA (P39) among European isolates burgdorfer sensu lato and influence of interspecies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98010210; PubMed-9350727;
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burgdorferi.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Pfam; PF02608; Bmp; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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145:309-314(1996).
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Best Local Sim
Matches 101;
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01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
CD4+ T cell-stimulating antigen precursor.
              Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget (
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson I.
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Waddueno E., Maltournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos H., Perez-Diaz J.-C., Purcell F.
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Webland J., Cossart P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _LISIN
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CLIP 11262 / Serovar 6a;
MEDLINE-21537279; PubMed-11679669;
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NCBI_TaxID=1642;
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Pred. No. 0.00037;
8; Mismatches 124;
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                                                                                                                                                                                                                                                                                                                                                                                                           Listeria
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-> A (IN STRAIN 212).

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-> P (IN REF. 3).
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Best Local Sim
Matches 101;
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031362;
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15-DEC-1998 (Rel. 37, I
15-DEC-1998 (Rel. 37, I
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LIPID
SEQUENCE
                                                                      Borrelia ç
Bacteria;
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SIGNAL
                                                                                               BMPB
                                                                                                         Basic membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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SIMILARITY: BELONGS
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Membrane; Lipoprotein; Signal;
PROBABLE.
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Pred. No. 0.
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SEQUENCE FROM STRAIN-PBI;

N.A.

MEDLINE-98010210;

D.,

Hauser

PubMed-9350727; er U., Wilske B.;

Bacteria; Spirochaetales; NCBI_TaxID=29519;

Spirochaetaceae;

Borrelia

garinii.

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RESOLT TCSALL ID AC OF CONTROL OF
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Best Local 9
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                                                                                                                                                                                           048754;
15-DEC-1998 (Rel. 37, Created)
01-MAR-2002 (Rel. 41, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
CD4+ T cell-stimulating antigen precur
TCSA OR LM01388.
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TCSA_LISMO
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                                                                                                                         Listeria monocytogenes.
Bacteria; Firmicutes; Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00013;
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                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLSGFQHGDAFTRWLKIPENKQLFTEKNIIILG-IDWIDTENVIPTGRYINLTYKTEEAG
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     PubMed=11679669;
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15 N
37236 MW;
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                                                                                                                              group;
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5; Mismatches
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Pred. No. 0.0013;
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N-ACYL DIGLYCERIDE (PROBABLE).
; 442BEF0BFEDDOC9A CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLE
                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                              Listeria.
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                                                                                                                                                                                                                                precursor
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                                                                                                                                                                                                                                                                                                                                                            357
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                                                                                                                                                      group;
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Baguero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Gobel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-252 FROM N.A.
STRAIN-85E0-1167;
MEDLINE-96096448; PubMed-7500019;
Sanderson S., Campbell D.J., Shastri N.;
"Identification of a CD4+ T cell-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listilist; LMO01388;
InterPro; IPR003760;
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                               294
                                                                                                                            169
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Exp. Med. 182:1751-1757(1995).
SUBCELLULAR LOCATION: Attached to the
                                                                                                                                                                                                                                                                                                                     ILGACGSSSDDKKSSDDKSSKDF--TVAMVTDTGGVDDRSFNQSAWEGLQKFGKANDMEK
                                                                                                                                                                                                                                                                                                                                      ISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALT----
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                                                             DKGQQIASSMYSSGVDVIFHAAGGTGNGVFAE-AKNLKKKDPSRAVWVIGVDRDQWDEGK
                                                                                                                            KVGFVGGVKGTVIDRFEAGFTAGVKA--
                                                                                                                                               AIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQ---DTSTK
                                                                                                                                                                                                                                                       GTDGYNYLQSASEADYK-----TNLNTAVRSDYDLIYGIGYKLKDAIEEVSKQKPKNQF
                                                                                                                                                                                                                                                                                    GGEITSVDSSTAELEGKYSSLANTNKNVWVLS-----GFQHGDAETRWLK-IPENKQ
VTANDGKDYNVTLTSEIKRVDIAV----
                             -SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSATVYLGIKD
                                                                                             ERLEQIASKDKPS----TLLAVAGPLTEIFSDIIANQNDR-----
                                                                                                                                                                                                                      LFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF02608; Emp; 1.
PF02608; Emp; 1.
PF0260013; PROKAR_LIPOPROTEIN; 1.
PF0600013; PROKAR_LIPOPROTEIN; 1.
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1 22 PR
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23
357 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROBABLE.
CD4+ T CE
                                                                                                                                                                                                                                                                                                                                                                                                 Score 168; DB 1;
Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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EDLAT ----
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RAKAGDFPGGTK - - - IEYGLDK
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MEDLINE-98010210; PubMed-9350727;
Roessler D., Hauser U., Wilske B.;
"Heterogeneity of EmpA (P39) among European isolates
burgdorferi sensu lato and influence of interspecies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DMPA_BORAF STANDARD; PRT; 339 AA.
031280; 031281; 031282; 031283;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
18-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                               LIPID
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02608; Bmp; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X81516; CAA57236.1; -. EMBL; X97237; CAA65876.1; -. EMBL; X97239; CAA65878.1; -. EMBL; X97241; CAA65880.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                   165
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TEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNS:| :| | | | | | | | | | | |
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                                                                           TNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYK 164
                                                                                                                                        GLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYSSLAN 104
                                                AGSNLIWLIGYKFSDV-AKAVSLQNSEMKYAI-----IDPVYSNEPIP-ANLVGMTFR
                                                                                                           GIPKVSLVIDGTFDDKSFNESALNGVKKLKEEFEIELVLKESSTNSYLSDLEG----LKD 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probable).
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                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         Membrane; Lipoprotein;
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llarity 23.3%;
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83
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PROBABLE.

BASIC MEMBRANE PROTEIN A.

N-ACYL DIGLYCERIDE (PROBABLE)

A -> S (IN STRAIN PLE).

I -> T (IN STRAIN PLJ7).

A -> P (IN STRAIN PLJ7).

I -> F (IN STRAIN PLJ7).

I -> F (IN STRAIN PLJ7).
                                                                                                                                                                     Score 166; DB
Pred. No. 0.007
68; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R. Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Havan Yugt R., Palmer N., Adams M.D., Gocayne J.D., Weddman J. Utterback T., Watthey L., McDonald L., Artiach P., Bowman C. Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatsger G., Cotton M.D., Hatsger G., Cotton M.D., Horst K., Roberts K., Hatsger G., Cotton M.D., Horst K., Roberts K., Hatsger G., Cotton M.D., Hatsger G., Cotton M.D., Hatsger G., Cotton M.D., Hatsger G., Cotton M.D
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-sih
                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          burgdorferi.";
Nature 390:580-586(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC 35210
MEDLINE-98065943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96178617; PubMed-8606088;
Ramamoorthy R., Povinelli L., Philipp M.T.;
"Molecular characterization, genomic arrangement, bmpb, a new member of the bmp class of genes encoproteins of Borrelia burgdorferi.";
Infect. Immun. 64:1259-1264(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Basic membrane protein BMPD OR BB0385.
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15-DEC-1998
                                                        InterPro; IPR003760;
                                                                                TIGR; BB0385;
                                                                                                         EMBL; U35450; AAC43984.1; -
EMBL; AE001144; AAB91505.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genomic sequence of a Lyme
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CHAIN
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Q45010; P94249; Q44857;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
   SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayt.
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey
Lathigra R., Tomb J.-F., Fleischmann R.D., Richardson
Dougherty B., Tomb J.-F., Consens T. D. Weidm
Peterson J., Kerlavage A.R., Quackenson T. D. Weidm
                                                                                                           MEDLINE=97132632; PubMed=8978084;
Aron L., Toth C., Godfrey H.P., Cabello F.C.;
"Identification and mapping of a chromosomal gene burgdorferi containing genes expressed in vivo.";
FEMS Microbiol. Lett. 145:309-314(1996).
                                                                                                                                                                                                              Simpson W.J., Cieplak W., Schrumpf M.E., "Nucleotide sequence and analysis of the encoding the immunogenic P39 antigen."; FEMS Microbiol. Lett. 119:381-388(1994).
                                                                                                                                                                                                                                                  MEDLINE-94327086; PubMed-8050720; Simpson W.J., Cieplak W., Schrump
                                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; (
                                                                                                                                                                                                                                                                                                                                                                 Basic membrane protein A precursor
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                                                                                                                                                                                       FROM N.A
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341
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25.1%;
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Pred.
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N-ACYL DIGLYCERIDE (PROBABLE).
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lickey E.K.
ardson D.,
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Best Local
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VARIANT
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-i- FUNCTION: NOT KNOWN; IMMUNOGENIC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Utterback T., Watth
Garland S., Fujii C
Smith H.O., Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-95111614; PubMed-7812434; Ojaimi C., Davidson B.E., Saint-G
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
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                       286
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407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS
                                                                                                                                                                                     YANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTD
                                                                                                                                                                                                                              GTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYSSLANTNKNVWVLSG
                                                                                                                                          KI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQ--NDRYL
                                                                                                                                                                                                                YRFSDVAKVAALQNPDMKYAI------
                                                                                                                                                                                                                                                              GTFDDKSFNESALNGVKKVKEEFKIELVLKESSSNSYLSDLEG----LKDAGSDLIWLIG
DKQQESLDKLITD
                       YGLKEGVVGFV--
                                            LGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQP
                                                                     IGVDEDQAYL --- APDNVITSTTKDVGRAL-
                                                                                           IGVDTDQSLYYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVY
                                                                                                                  YIGSFADLEAGRSVATRMYSDEID-----
                                                                                                                                                                                                                                                                                                                                                                                                                                           PF02608; Bmp; 1.
TE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  вв0383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U49938; AAC44712.1;
AE001143; AAC66757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L24194; AAA72406.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L35050; AAC41401.1;
                                                                                                                                                                                                                                                                                                                85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390:580-586(1997).
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                         Membrane; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003760;
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339 /
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                                                                                                                                                                                                                                                                                                             Score 161; DB
Pred. No. 0.00
58; Mismatches
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F -> S (IN STRAIN 297)
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BASIC MEMBRANE PROTEIN
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Horst K., Roberts
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Best Local S
Matches 90
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Reessign D., Hauser U., Wilske B.;
"Heterogeneity of EmpA (P39) among European isolates burgdorferi sensu lato and influence of interspecies serodiagnosis.";
Telia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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031284;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Membrane;
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PROSITE; PS00013; PRO
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NCBI_TaxID=29518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Basic membrane protein
    337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003760;
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15-DEC-1998 (Rel.
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    EFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEE
                                                                                  EYSNSFSDIDIARVMANKMYSKGIDIIHFAA--GLAGVGVIEAPKEL
                                                                                                           KNSDKKTKITTDKIEIN----LGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSD
                                                                                                                                       GAFLAGY----IAAKKSVS----
                                                                                                                                                                AGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWN-----L
                                                                                                                                                                                                                     VLSGFQHGD-AFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVIPTGRYINLTYKTEE 167
                                                                                                                                                                                                                                                GVLDDKSFNSSANEALLRLKKDFPENIEKVFSSA--VSGVYSSYVSDLDNLKMNGSGLIW 93
                                                                                                                                                                                                                                                                          GTVNDNSFNQSGWEAIQQLGALTGGEITSVDSSTAELEGKYSS----LANTNKN----VW 110
                                                       IIANQNDRYLIGVDTDQSLYYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGF
                                                                                                                                                                                            *LVGYMLADVSLSVSLENPE----INYGIIDPIYGDDVQIPKNL----IGVVFRIEQ
                                                                                                                                                                                                                                                                                                       90;
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microbiol. 35:2752-2758(1997). ELLULAR LOCATION: Attached to the membrane by a lipid
                             GDGYYVIGADQDQSHLAPK---NFITSVIKNVGDALYLITSE----
                                                                                                                                                                                                                                                                                                                                                                                                                          Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                         341 AA;
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                                                                                                                                                                                                                                                                                                                                                                       15
37198 MW;
                                                                                                                                                                                                                                                                                                                 7.18;
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Last annotation update)
n B precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Signal
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                                                                                                                                                                                                                                                                                                                                                                      BASIC MEMBRANE PROTEIN B.
N-ACYL DIGLYCERIDE (PROBABLE).
; 1E8EA3E3D54ACDB1 CRC64;
                                                                                                                                                                                                                                                                                                                 Score 153;
Pred. No. 0.
                                                                                                                                      SKIGFIGGVKGDIVDAFRYGYEAGAKYANKGIEIVS
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Y040_MYCGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96026346; PubMed-7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J. Fritchman J.L., Weldman J.F., Small K.V., Sandusky M., Fuhrmann Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucler T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U39683; AAC71256.1; -. EMBL; U02125; AAD12400.1; -. TIGR; MG040; -.
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"A survey of the Mycoplasma
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AR LOCATION: Attached
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Hu P.-C., Bott K.F., Hutchison
he Mycoplasma genitalium genome
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15-DEC-1998 (Rel. 37, Created)
T 15-DEC-1998 (Rel. 37, Last sequence updatation updata
                                                                                STRAIN-ATCC 35210 / B31;

MEDLINE-98065943; PubMed-9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman Utterback T., Watthey L., McDonald L., Artiach P., Bowman Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., H smith H.O., Venter J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97132632; PubMed=8978084;
Aron L., Toth C., Godfrey H.P., Cabello F.C.;
"Identification and mapping of a chromosomal ge
burgdorferi containing genes expressed in vivo.
FEMS Microbiol. Lett. 145:309-314(1996).
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                       Nature 390:580-586(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and DNA sequence analysis of bmpC, potential membrane lipoprotein of Borrelia
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                        SEQUENCE FROM N.A.
MEDLINE-87260937; PubMcd-3037534;
Laddaga R.A., Chu L., Misra T.K.,
"Nucleotide sequence and expressions."
                                                                                                                                                                                                               Staphylococcus aureus Plasmid pI258.
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P08663;
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-I- FUNCTION: RESISTANCE TO HG(2+) IN BACTERIA APPEARS TO BE GOVERNED BY A SPECIALIZED SYSTEM WHICH INCLUDES MERCURIC REDUCTASE. MERA PROTEIN IS RESPONSIBLE FOR VOLATILIZING MERCURY AS HG(0).

-I- CATALYTIC ACTIVITY: Hg + NADP(+) + H(+) - Hg(2+) + NADPH.

-I- COPACTOR: FAD.

-I- SUBUNIT: HOMODIMER.

-I- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.
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PRINTS; PR00411; PNDRDTASEI.
PROSITE; PS01047; HMA_1; 1.
PROSITE; PS50846; HMA_2; 1.
PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00403; HMA; 1.
Pfam; PF00070; pyr_redox; 1.
Pfam; PF02852; pyr_redox_dim; 1.
PRINTS; PR00368; FADPNR.
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InterPro; IPR001934; HMA.
InterPro; IPR000815; Hg_reductase.
InterPro; IPR001100; pyr_redox.
InterPro; IPR004099; pyr_redox_dim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - 1 - SIMILARITY: CONTAINS 1 HMA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SIMILARITY: BELONGS TO :
OXIDOREDUCTASES CLASS-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mercuric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
279
                                     257
                                                                                                               199
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                                                                                                                                                                                                                                                                  106
                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                             10
                                   GSGYIAAELGQMFHNLGTEV---TLMQRSERLFKTYDPEISEAIDESLTEQGLNLITGVT
                                                                                                                                                LAKKF----PSDPTKRSAIVIGGGISPAVTDFIAG-----YLAGIKAWNLKNSDKKTKI-
                                                                                                                                                                                                                             LKIPENK ----
                                                                                                                                                                                                                                                              ENGAKVAMVERGTVGGTCVNIGCVPSKTMLRAGEINGLAQNNP----FTGLQTSTGAADL 161
                                                                                                                                                                                                                                                                                                   QSGWEAIQQLGALTGG---EITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRW 124
                                                                                                                                                                                                                                                                                                                                        ELSDDQIEKAKQNISAAGYQPGEEESQPSENSVDFNRDGDYDLLIIGSGGAAFSAAIKAN 105
                                                                                                                                                                                                                                                                                                                                                                             EKSADNQNKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSF--N 67
                                                                    -----TTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDII----
                                                                                                           IDDKTIQVNGQNITSKS-FLIATGASPAVPE-IPGMNEVDYLTSTSALELKEVPQRLAVI 256
                                                                                                                                                                                       AQLTEQKDGLVSQMRQEK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        resistance; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                         -QLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pyr_redox_dim.
-- IGVDTDQSLVYTKTKNKFFTSILKNLGYSV--
                                                                                                                                                                                                                                                                                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 136; DB 1
Pred. No. 0.26;
64; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REDOX-ACTIVE.

FAD (FLAVIN PART) (B'HG(2+) (POTENTIAL).

HG(2+) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAD (ADP PART) (PROBABLE).
                                                                                                                                                                                     -----YIDL---IEEYGFDLIRGEASF 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOBEASECFA99C049 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flavoprotein; FAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions ng as its content is in wed. Usage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Length 547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid.
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                                                                                                                                                                                                                                                                                                                                                                                                                  96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus pyogenes. Proc. Natl. Acad. Sci. U.S.A. 98.4658-4663(2001).

-1- CATALYTIC ACTIVITY: DIPEPTIDE + H(2)0 - 2 AMINO ACID.

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY U34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-SF370 / ATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probable dipeptidase B (EC PEPDB OR SPY2066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEDB_STRPY
Q99XS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE006627; AAK34726.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SF370 / ATCC 700294 / Serotype MEDLINE-21192684; PubMed-11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pyogenes.
                                                              226
                                                                                                                                                                                    172
                                                                                                                                                                                                                                                                                                          113
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LAGIKAWNLKNSDKKTKIT
                                                                                                                                                                                                                                                                                                                                                                  NMAIVTAGGTVND-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KETTKEEKSADNQN------KQITDVSKISGLVNERKSEIMAAKADANKHFGL 50
                                                              ASEDVEKVAKKAKSYTEVDGKFH---TAKSYNPPLNDANRSRSFSG-----
                                                                                                                                                                                 GNIVTLADKD-GIWYMEILSGHQYVA----IKFPDDKYAVFPNTFYLGHVDFNDKENTI
                                                                                                                                                                                                                                         GKYSSLANTNKNVW---VLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVI 153
                                                                                                                                                                                                                                                                                                                                                                                                                          KDNPAGEKWKDLSNGFEYPLPEHSYRYSAIPDVTPNKGVYDE------AGFNE-FGV 112
                                                                                                                                                                                                                                                                                                SMS-ATVSASANDAIQKIDPYVKNGLAESSMTSVILPSVKTAREGVALIAKIVTEKGAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATVGLTEQQAKEKGYDVKTSVLPLDAVPRAL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYTKKSNSRNLAGFEFGKKSATVY-----
                                                                                                                      PTGRYINLTYKTEEAGWLAGYANASFLAKKF--PSDPTKRSAIVIGGGISPAVTDFIAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATEAISE---AKKEFEEKTKTIPAEEVRKTL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EYLQTSNNRIYAAGDVTLGPQFVYVAAYEGGIVANNALGLAKRKIDLRFVPGVTFTNPSI 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YQKVEQNGKSTSIYIEVNGQEQVIEADQVLVATGRKPNTETLNLESAGVKTGKKGEVLTN 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dipeptidase; Co
498 AA; 55499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.0%;
20.5%;
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Last annotation updat
B (EC 3.4.-.-).
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99 MW; B9394DC94C19AE4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                                                                                                                           NSFNQSGWEAIQQLGALTGGE----ITSVDSSTAELE 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 129; DB Pred. No. 0.61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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TDKIEINLGFDVQDTSTKER---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 498;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 144;
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Search completed: July 18, 2002, 15:30:21 Job time: 68 sec

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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2155
1 MWDKETTKEEKSADNONKQI......KQPDXQQUSLDKLITDINNL 423
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Copyright (c) 1993 - 2000 Compugen Ltd.
          sp_organelle:*
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sp_invertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

Result No.	Score	Query Match	% Query Match Length DB	BU	ID	Description
1	693.5	32.2	457	2	Q48902	Q48902 mycoplasma
N	552	25.6	461	16	Q98QL5	Q98q15 mycoplasma
ω	391	18.1	465	N	Q9X775	Q9x775 mycoplasma
4	384.5	17.8	428	N	052311	052311 mycoplasma
G	382.5	17.7	428	N	Q9RGX5	
6	379.5	17.6	428	N	032417	032417 mycoplasma
7	379	17.6	429	Ŋ	Q9RGX6	_
8	379	17.6	429	ν	Q9RGX4	_
9	377.5	17.5	428	N	Q9RGX7	
10	374.5	17.4	428	N	Q9RGX3	Q9rgx3 mycoplasma
11	373.5	17.3	428	ຎ	Q9R3N6	Q9r3n6 mycoplasma
12	228	10.6	349	N	Q9EV91	Q9ev91 clostridium
13	220.5	10.2	350	16	Q99ZH4	Q99zh4 streptococc
14	203.5	9.4	350	16	Q9CFM9	Q9cfm9 lactococcus
15	202	9.4	350	16	Q97RH0	Q97rh0 streptococc
16	192	8.9	357	16	Q97L60	

5	44	43	42	41	40	39	38	37	36	35	34	ű	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
126.5	127	127	131.5	132	132.5	133.5	134	137.5	140	143	143.5	145	148	150	156	157	160	161	161	162.5	164	168	168.5	170	173	174	178.5	182
5.9	5.9	5.9	6.1	6.1	6.1	6.2	6.2	6.4	6.5	6.6	6.7	6.7	6.9	7.0	7.2	7.3	7.4	7.5	7.5	7.5	7.6	7.8	7.8	7.9	8.0	8.1	8.3	8.4
894	2045	912	1558	326	330	1786	539	889	379	353	243	264	329	524	325	339	325	339	339	525	347	341	516	264	357	342	359	348
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Q9L962	Q9A0K5	Q9XD52	096275	Q92X35	Q926D6	Q9U0P0	Q9PQ10	Q9L961	Q9RSQ4	Q93V09	031361	031359	Q98GW4	Q9PRC9	Q9R777	Q9FD92	Q9R776	087960	Q9S6C1	Q9PQR5	Q9AK42	Q9FD93	Q9PRD3	031358	Q92BW7	Q9A1P7	Q9WXV7	Q9AK41
Q91962 moraxella c	Q9a0k5 streptococc		O96275 plasmodium	Q92x35 rhizobium m	Q926d6 rhizobium m	Q9u0p0 plasmodium	Q9pq10 ureaplasma	Q91961 moraxella c	Q9rsq4 deinococcus	Q93v09 borrelia bu	031361 borrelia ga	031359 borrelia ga	Q98gw4 rhizobium l	Q9prc9 ureaplasma		borrelia	borrelia	borrelia	Q9s6cl borrelia bu	Q9pqr5 ureaplasma	Q9ak42 streptomyce	Q9fd93 borrelia bu	Q9prd3 ureaplasma	ā	Q92bw7 listeria in		Q9wxv7 thermotoga	Q9ak41 streptomyce

ALIGNMENTS

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65 SFNQSGWEAIQQLGALTG-GEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGD 119	5 ETTKEEKSADNQNKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDN 64	vative 81; Mismatches 141; Indels 41; G	Query Match 32.2%; Score 693.5; DB 2; Length 457;	NCE 457 AA; 50789 MW;	SIGNAL 1 25 POTENTIAL. CHAIN 26 457 AG 243-5 PROTEIN.		Pfam; PF02608; Bmp; 1.	InterPro; IPR003760; Bmp.	EMBL; D16674; BAA04082.1;	Microbiol. Immunol. 39:393-400(1995).	sequence.";	te nucleo	"Metastatic promoting activity of a novel molecule, Aq 243-5 derived	,	Ushio S., Iwaki K., Taniai M., Ohta T., Fukuda S., Sugimura K.,	MEDLINE-96163149; PubMed-8551970;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=2094;	Mycoplasmataceae; Mycoplasma.	Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;	Mycoplasma arginini.	OTEIN PRECURSOR.	(TrEMBLrel, 19, Last	(TrEMBLrel, 01,	01-NOV-1996 (TrEMBLrel. 01, Created)	FREEHMANNA, FRA	OAROOD DEET.TWINDER. DET. 457 AA	JLT 1	
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RESULT
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Best Local S
Matches 133
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Nucleic Acids Res. 29:2145.
EMBL; AL445564; CAC13519.1;
MypuList; MYPU_3460; -
InterPro; IPR003760; Bmp.
Pfam; PF02608; Bmp; 1.
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SEQUENCE
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STRAIN-UAB CTIP;
MEDLINE-21267165; PubMed-11353084;
Chambaud I., Hellig R., Ferris S., B.
Moszer I., Dybvig K., Wroblewski H.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2001 (TIEMBLIEL. 18, Created)
01-OCT-2001 (TIEMBLIEL. 18, Last sequence update)
01-OCT-2001 (TIEMBLIEL. 18, Last annotation updat
ABC TRANSPORTER XYLOSE-BINDING LIPOPROTEIN.
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Q98QL5;
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NCBI_TaxID=2107;
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Local Similarity 31.2%;
les 133; Conservative (
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        NVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTEN-VIPTGRYINLTYKTE
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                                                                                                                     NDNSFNQSGWEAIQQLGALTGGEITS----
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9e-24;
les 161;
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Query Match
Best Local Similarity
Matches 119; Conserv
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
P48 MEMBRANE LIPOPROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003760; Bmp. Pfam; PF02608; Bmp; 1. Signal; Lipoprotein. SIGNAL 1 22
                                                                                                                                                                                                                                                                                                                                                                                                           malp product of Mycoplasma ferment
of bacterial lipoproteins.;
Infect Immun. 67:6213-6216(1999).
EMBL; AJ132423; CAB43718.1; -.
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Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasmataceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "P48 major surface antigen of Mycoplasma agalactiae is
                                 186
 212
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                            LAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPL-
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                                                                                                                                                              ITDEGSVHDESFNQSGWEAVHKVSYELGLDKAQV-SGNKNLRNKVYEPKKGQLLEAYKNA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRKTLE
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                                                                                               IDSGFRYIVLCGFTHQASL---VGLDENYIKKIKDNNIIFITVDFNLFTEDDANVKTFIK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDRFIVGVDTDQSLSFTNDSKRFFTSIVKNIAFPVYQILLALLTKDEESVILKEGNDKFL
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                                                                                                                                                                                                                                                                                                            23
465 AA;
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                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                              22
465 P
51149 MW;
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                                                                                                                                                                                                                              Score 391; DB 2;
Pred. No. 5.9e-15;
6; Mismatches 128
                                                                                                                                                                                                                                                                                                            P48 MEMBRANE LIPOPROTEIN. 60AD5448CFE03C96 CRC64;
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Matches 116
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052311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rawadi G., Dyer K., Dujeancourt A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF036106; AAB99740.1; -.
InterPro; IPR003706; Bmp.
Pfam; PF02608; Bmp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma fermentans.
Bacteria; Firmicutes; Bacillus/Clostridium
Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TIEMBLIEL 06, 01-JUN-1998 (TIEMBLIEL 06, 01-JUN-2001 (TIEMBLIEL 17, MEMBRANE LIPOPROTEIN P48V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipoprotein SEQUENCE '
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SLDKLITDIN
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                                                                                                                                                                      ILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFG:
                                                                                                                                                                                                                  FFTSILKNLGYSVFSVLSDL-----YTKKSNSRNLAGFEFGKKSATVYLGIKDRF
                                                                                                                                                                                                                                                                                                                                                                  SFGGGAFPGVTTFNEGFAKGILYYNQKH--KSVKFTHTSPVKLDSGF----TAGEKMNT
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                                                                     IGVAENHFSNTEEQAKINNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSE
                                                                                                                   VDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQE
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Pred. No. 1.3e-14;
6; Mismatches 157;
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Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.J., Kim M.J., Kim M.J., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.J., Kim M.J., Kim M.J., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.J., Kim M.J., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.J., Kim M.J., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.J., Kim M.J., Muhlradt P.F., Wise K.S.;
Cilcutt M.J., Kim M.J., Kim M.J., Muhlradt P.F., Kim M.J., Muhlradt P.F., Mu
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NCBI_TaxID=2115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNDESNISFKEKDISKYTTTNANGKQVVKNAELLKLKPVLITDEGKIDDKSFNQSAFEAL
                                                                                                                                                                                                              VDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFGGGAFPGVTTFNEGFAKGILYYNOKH--KSSKIYHTSPVKLDSGF----TAGEKMNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERNQIKIIGIDE-DIETEYKW--FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVA
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RLEAIISAIN 424
                                                                   SLDKLITDIN
                                                                                                                                                                                                                                                                                     ILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFGTQ
                                                                                                                                                                                                                                                                                                                                                                                                                            VINNVLSSTPADVKYNPHVILSVAGPAT--FETVRLANKGQYVIGVDSDQGMI--QDKDR
                                                                                                                                          IGVAENHFSNTEEQAKINNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSE
                                                                                                                                                                                                                                                                                                                                                    FFTSILKNLGYSVFSVLSDL------YTKKSNSRNLAGFEFGKKSATVYLGIKDRF
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428 AA;
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(TTEMBLTel. 13, Last sequence update)
(TTEMBLTel. 17, Last annotation update)
aCTIVATING LIPOPROTEIN-404 PRECURSOR.
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47835 MW;
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27.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 382.5; DB 2; Pred. No. 1.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.

MACROPHAGE ACTIVATING LIPOPROTEIN-404;

D03F0F47EA2B1460 CRC64;
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032417;
01-JAN-1998
01-JAN-1998
01-JUN-2001
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Matsumoto M., Seya T.;
Submitted (APR-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent number JP1997157295-A/1
17-JUN-1997. KAGAKU GIJUTSU SH
EMBL; D64083; BAA22530.1; -.
EMBL; AB026157; BAA77211.2; -.
Interpro; IPR003760; Bmp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M161Ag, a Mycoplasma fermentans gene product production by human monocytes.";
J. B101. Chem. 273:12407-12414(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98022661; PubMed=9359703; Matsumoto M., Takeda J., Inoue N., Hara T., Ha Nagasawa S., Akedo H., Seya T.; "A novel protein that participates in nonself malignant cells by homologous complement."; Nat. Med. 3:1266-1270(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycoplasma fermentans.
Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98241611; PubMed=9575196;
Matsumoto M., Nishiguchi M., Kikkawa
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NCBI_TaxID=2115;
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VINNVLSSTPADVKYNPHVILSVAGPAT - - FETVRLANKGQYVIGVDSDQGMI -
                                                                                                            IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK 303
                                                                                                                                                                                                                      VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ
                                              FFTSILKNLGYSVFSVLSDL-----
                                                                                                                                                                            SFGGGAFPGVTTFNEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----
                                                                                                                                                                                                                                                                    ERNQIKIIGIDF-DIETEYKW--FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVA
                                                                                                                                                                                                                                                                                                                                                           KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL
                                                                                                                                                                                                                                                                                                                                                                                                     QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNDESNISFKEKDISKYTTTNANGKQVVKNAELLKLKPVLITDEGKIDDKSFNQSAFEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NERKSEIMAAKADANKH---
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NCE 428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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26.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 379.5; DB 2
Pred. No. 2.4e-14;
8; Mismatches 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----FGLNMAIVTAGGTVNDNSFNQSGWEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F43B078F21DADD6E
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                                           YTKKSNSRNLAGFEFGKKSATVYLGIKDRF
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                                                                                       -QDKDR
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Best Local Similarity
Matches 117; Conserv
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-INCCONITUS;

MEDLINE-9911554; PubMed=9916088;

Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;

Tolferential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopeptide of Mycoplasma formentans.*;

Infect. Immun. 67:760-771(1999).

EMBL; AF099210; AAD16394.1; -.

InterPro; IPR003760; Emp.

Pfam; PF02608; Emp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal; Lipoprotein.
SIGNAL 1
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                           NERKSEIMAAKADANKH---
WIGVAENHFSNTEEQAKINNKIKEAIKMFKELPEDFVKYINSDKVLK---
                                                                                                   VINNVLSSTPADVKYNPHVILSVAGPAT -- FETVRLAANKGQYVIGVDSDQGMI--QDKD
                                                                                                                                                       SFGGGAFPGVTTFNEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNT
                                               RILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFGTQ
                                                                                                                  IAS-----KDKPSTLLAVAGPLTEIESDI-IANQNDRYLIGVDTDQSLYYTKTKN
                                                                                                                                                                                VIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQ 253
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                       FVDIADTSLEGNDKKL-ATEAISEAKKEF---
                                                                         KFFTSILKNLGYSVFSVLSDL-----
                                                                                                                                                                                                          ERNQIKIIGIDF-DIETEYKW--FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVA
                                                                                                                                                                                                                                    TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 194
                                                                                                                                                                                                                                                              KAINKQTGIEINNVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL
                                                                                                                                                                                                                                                                                        QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF 134
                                                                                                                                                                                                                                                                                                                 NNDESNISFKEKDISKYTTTNANGKQVVKNAELLKLKPVLITDEGKIDDKSFNQSAFEAL 86
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                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                    88; Mismatches
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                               Score 379; DB 2; Pred. No. 2.6e-14;
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MACROPHAGE ACTIVATING LIPOPROTEIN-404.

B6D09A8812AC3171 CRC64;
                                                                                                                                                                                                                                                                                                                                           ----FGLNMAIVTAGGTVNDNSFNQSGWEAI 74
                                                                        YTKKSNSRNLAGFEFGKKSATVYLGIKDR 352
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                        EEKTKTIPAEEVRKTLEIPEMPDKQPD
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DGNKID
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Best Local Similarity 26.9
Matches 116; Conservative
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Q9RGX4;
Q9RGX4;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-9911554; PubMed-9916088; Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.; Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.; "Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopeptide of Mycoplasma fermentans."; Inject. Immun. 67:760-771(1999).
EMBL; AF099212; AAD16396.1; -.
InterPro; IPR003760; Emp.
Pfam; PF02608; Bmp. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal; Lipoprotein. SIGNAL 1
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NCBI_TaxID=2115;
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Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFGGGAFPGVTTFNEGFAKGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNDESNISFKEKDISKYTTTNANGKQVVKNAELLKLKPVLITDEGKIDDKSFNQSAFEAL
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NVSERLEATISAIN
                                                                                                              WIGVAENHFSNTEEQAKINNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVS
                                                                                                                                                                                                                             RILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKDKKADKKWSHFGTQ
                                                                                                                                                                                                                                                                                   KEFTSILKNLGYSVFSVLSDL------YTKKSNSRNLAGFEF(KKSATVYLGIKDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI
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                                                  ESLDKLITDIN
                                                                                                                                                                    FVDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTIPAEEVRKTLE::PEMPD-KQPDKQQ
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429 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 379; DB 2;
Pred. No. 2.6e-14;
9; Mismatches 154
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MACROPHAGE ACTIVATING LIPOPROTEIN-404;

B6D08CF975AC3171 CRC64;
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RESULT
Q9RGX7
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Q9RGX3
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Best Local S
Matches 110
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Q9RGX7;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-II-29/1;
MEDLINE-99115554; PubMed-9916088;
MEDLINE-99115554; PubMed-9916088;
Calcutt M.J., Kim M.F., Karpas A.B., Muhlra
"Differential posttranslational processing
variation of a major surface lipoprotein an
lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-771(1999).
EMBL; AF099209; AAD16393.1; -.
           Q9RGX3 PRELIMINARY; PRT; 428 AA.
Q9RGX3;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-JUN-2001 (TrEMBLrel. 13, Last sequence up
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation
MACROPHAGE ACTIVATING LIPOPROTEIN-404 PRECUE
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Pfam; PF02608; Bmp; 1.
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mes 110; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                    WVLNGFKHQQSIKQY--IDAHREELERNQIKIIGIDF-DIETEYKW--FYSLQFNIKESA
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                                                                                                                                                PEDFVKYINSDKALKDGNKIDNVSERLEAIISAIN
                                                                                                                                                                         PAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDIN
                                                                                                                                                                                                                                                        LANKGQYVIGVDSDQGMI--QDKDRILTSVLKHIKQAVYETLLDLILEKEEGYKPYVVKD
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                                                                                                                                                                                                                                                                                                            YHTSPYKLDSGF----TAGEKMNTYINNYLSSTPADYKYNPHYILSVAGPAT--FETYR
                                                                                                                                                                                                                                                                                                                          -TTDKIEINLGFDVQDTSTKERLEQIAS------KDKPSTLLAVAGPLTEIFSDII
                                                                                                                                                                                                                                                                                                                                                                                          WLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGIKAWNLKNSDKKTKI
                                                                                                                                                                                                    KKADKKWSHFGTQ-----
                                                                                                                                                                                                                             NSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEAISEAKKEFEEKTKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 (TremBLrel. 13, Created)
0 (TremBLrel. 13, Last sequence update)
1 (TremBLrel. 17, Last annotation updata
acTIVATING LIPOPROTEIN-404 PRECURSOR.
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428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                  KEKWIGVAENHFSNTEEQAKINNKIKEAIKMFKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 377.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.

MACROPHAGE ACTIVATING LIPOPROTEIN-404

, D6B69C0BA969CFE1 CRC64;
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Mismatches 146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428
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PRECURSOR

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Best Loc
Matches
                                                                  Q9R3N6;
01-MAY-2000
01-MAY-2000
01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Lipoprotein.
SIGNAL 1 2
CHAIN 25 42
SEQUENCE 428 AA; 4
Mycoplasma fermentans.
Bacteria; Firmicutes; Bacillu
Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2115;
[1]
                                                MALP.
                                                         LIPOPROTEIN
                                                                                                         Q9R3N6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
"Differential posttranslational processing confers intraspecies
"ratiation of a major surface lipoprotein and a macrophage-activating
lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-771(1999).
EMBL, AF099213; AAD16397.1; -.
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Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99115554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cal Similarity
115; Conserv
                                                                                                                                                                            SLDKLITDIN
                                                                                                                                                                                                                                   FFTSILKNLGYSVESVLSDL-----YTKKSNSRNLAGFEFGKKSATVYLGIKDRF
                                                                                                                                                                                                                                                                         VINNVLSSTPADVKYNPHVILSVAGPAT -- FETVRLANKGQYVIGVDSDQGMI--QDKDR
                                                                                                                                                                                                                                                                                    IAS-----KDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNK
                                                                                                                                                                                                                                                                                                                                                                                                       QQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NERKSEIMAAKADANKH------FGLNMAIVTAGGTVNDNSFNQSGWEAI
                                                                                                                                                                                                                                                                                                              SFGGGAFPGVTTENEGFARGILYXNQXH--KSSKIYHTSPVKLDSGF----
                                                                                                                                                                                                                                                                                                                                                                       TEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI 194
                                                                                                                                                                                                                                                                                                                                                                                          KAINKQTGIEINSVEPS-SNFESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREEL
                                                                                                                                                                                               IGVAENHFSNTEEQAKINNKIKEAIKMFKE----LPEDFVKYINSDKALKDGNKIDNVSE
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428
                                                       (TrembLrel. 13, Created)
(TrembLrel. 13, Last seq
(TrembLrel. 18, Last ann
MALP-404 PRECURSOR.
                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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M.F., Karpas A.
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47875
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26.78;
                             Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
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MACROPHAGE ACTIVATING LIPOPROTEIN-404;

C7A536B409A60132 CRC64;
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                                                                  sequence up
annotation
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No. 4.7e-14;
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                           group;
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                             Mollicutes;
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Best Loc
Matches
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Q9EV91;
01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-DEC-2001 (TrEMBLrel. 19, L
PUTATIVE SUBSTRATE BINDING LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal;
                                                                                                             Bacteria; Firmic Clostridium. NCBI_TaxID=1511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 variation of a major surface lipoprotein and lipopeptide of Mycoplasma fermentans."; Infect Immun 67:760-771(1999).

EMBL; AF100324; AAD25736.1; -.
EMBL; AF099214; AAD16398.1; -.
EMBL; AF099214; AAD16398.1; -.
InterPro; IPR003760; Bmp.
Pfam; PF0260B; Bmp; 1.
    SEQUENCE FF
STRAIN-DSM
                                                                                                                                                                                                                                                                                                                    TRANSPORTER.
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STRAIN-PG18, M39A, AND M70B;
STRAIN-PG18, M39A, AND M70B;
Calcutt M.J., Kim M.F., Karpas A.B., Muhlra
"Differential posttranslational processing
                                                                                                                                                                                                                                       Clostridium
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: Local Similarity
ches 115; Conserv
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01-JUN-2001
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Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an MI strain of Streptococcus pyogenes."; Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

EMBL; AE006563; AAK34087.1; ".
InterPro; IPR001114; Adenylsucc_synt.
InterPro; IPR001761; Peripla_BP_like.
InterPro; IPR001761; Peripla_BP_like.
InterPro; IPR000217; Tubulin.
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reductase and thioredoxinsystem from Clostridium sticklandii."
Arch. Microbiol. 175:8-18(2001).
EMBL; AJ276209; CAC14304.1; -.
InterPro; IPR003760; Bmp.
                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SF370 / ATCC 700294 / SEROTYPE M.
MEDLINE-21192684; PubMed-11296296;
Ferretti J.J., McShan W.M., Ajdic D.J.,
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                                                                                                                                                                                                                                                                                          (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                         (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                           pyogenes.
micutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
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Last sequence
Last annotation
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Pred.
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annotation
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No. 1e-05;
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lon update)
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                                                                                                                                       D.J.,
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                                                                                                                          J., Savic (
Lai H.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              391
                                                                                                                                                                                                                                                                                                                                                                                                                     342
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                                                                                                                                                                                                                                     Streptococcaceae;
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                                                                                                                          Lyon K.
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Best Local
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01-JUN-2001
01-OCT-2001
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Pfam; PF00533; Peripla Bp_like;
PROSITE; PS00227; TUBULIN; UNKN
Lipoprotein; Complete proteome.
SEQUENCE 350 AA; 36396 MW;
Complete
SEQUENCE
                                          Bolotin A., Wincker P., Mauger S., Jaillon O., Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic aclactic ssp. lactis III403.", Genome Res. 11.731-753(2001).
EMBL: AE006374: AAK05536.1; -.
Interpro; IPR003760; Emp.
Pfam; PF02608; Emp; 1.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-IL1403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9CFM9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9CFM9
                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BMPA
                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactococcus
                                                                                                                                                                                                                                                   MEDLINE=21235186; PubMed=11337471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 AAKADANKHEGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTG-GEITSVDSSTAELEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGYLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASKGGASGKTDLKVAMVTDTGGVDDKSFNQSAMEGLQSWGKEMGLQKGTGFDYFQSTSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKIKSGDIKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEFEEKTKTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGVFNEAKAINEKRSEADKVWVIGVDRDQKDEGKYTSKDGKEANFVLASSIKEVGKAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTEIFSDIIANQNDR-----YLIGVDTDQ--SLVYT----KTKNKFFTSILKNLGYSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNVASVTFADHEAAYLAGIAAAK-----TTKTKTVGFVGGMEGTVITRFEKGFEAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYA----TNLDTAVSGGYQLIYGIGFA--LKDAIAKAAGDNEGVKFVIID----DIIEGK
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1 (TrEMBLrel. 17,
1 (TrEMBLrel. 18,
  350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       lactis (subsp. lactis) (Streptococcus lactis).
irmicutes; Bacillus/Clostridium group; Streptoc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----VDDTIQVKVDYAGSFGDAAKGKTIAAAQYAAGAD--VIYQAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348
  36652 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 220.5;
Pred. No. 2.
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  24A30D8EEDD4C814 CRC64;
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                                                                                                                                                                                                                              Malarme
                                                                                                                                                                              bacterium
                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                 Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Query Match Best Local 9 Matches

97;

Conservative

63;

Mismatches

Indels

75;

Gaps

17;

Similarity

9.48;

Score 203.5; DB Pred. No. 0.00027

DB 16; 157;

Length

350;

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                                 Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                               MEDLINE-2337,209; PubMed-11463916;
Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D., Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L., McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey I. Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.; "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.";
                                                                                                            Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q97RH0
Q97RH0;
                                                                                                                                                                                                                   Science 293:498-506(2001).
EMBL; AE007390; AAK74976.1; -.
TIGR; SP0845; -.
                                                                                                                                      InterPro; IPR000217; Tubulin.
Pfam; PF02608; Bmp; 1.
PROSITE; PS00227; TUBULIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae.
Bactaria; Firmlcutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2001 (TrEMBLrel. 18, 01-OCT-2001 (TrEMBLrel. 18, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus
                                                                                                                                                                                        InterPro; IPR001114; Adenylsucc_synt.
InterPro; IPR003760; Bmp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SP0845
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33 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGA---LTGGEITSVD 89
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                                                                                               SILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDK 366
                                                                                                                                --IVYQVAGGTGAGVFAEAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVLV
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US-09-368-375-2
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Query Match Best Local Similarity Matches 98; Conserv	US-08-961-083-8 US-08-961-083-8 Sequence 8, Application US/ GENERAL INFORMATION: APPLICANT: Choi et. al. TITLE OF INVENTION: Str NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS: ADDRESSE: Human Geno STREET: 9410 Key West CITY: ROCKVILLE STATE: MATYLAND COUNTRY: USA ZIT: 20850 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: ASCII Text OPERATING SYSTEM: MSD SOFTWARE: ASCII Text CURENT APPLICATION NUMBER: UFILING DATE: FILING DATE: FILIN	28 108 5.0 29 108 5.0 30 108 5.0 31 107.5 5.0 32 107.5 5.0 34 107 5.0 35 107 5.0 36 107 5.0 37 107 5.0 39 107 5.0 40 107 5.0
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Length 328; 1; 15; Indels 84; Gaps 1	e Antigens and Vaccines	Sequence 16, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 184, Appli Sequence 184, Appli Sequence 4, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 10, Appli Sequence 10, Appli

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RESULT 2
US-08-396-957A-5
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                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/664,731
FILING DATE: 05-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,716
FILING DATE: 05-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                         TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SIMPSON, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 K----AVEDAKAKILDGSVKVP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
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                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/020,245 FILING DATE: 19-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/396,957A FILING DATE: 01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --IVYQVAGGTGAGVFAEAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIDDVIKDQKNV-----ASVTFADNESGYLAGVAAAK-----TTKTKQVGFVGGI 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSTAELE-----GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNII 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLATEAISEAKKEFEEKTKTIP 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STLKQVGTTVKDI-----SNKAERGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEGK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSTLLAVAGPL-TEIFSDIIANQNDR-----YLIGVDTDQSL--VYT----KTKNKFFT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESEVISRFEAGFKAGV-----ASVDPSIKVQVDYAG-SFG-DAAKGKTIAAAQYAAGAD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSTSEADYANNLQQAAGSYNLIFGV-----GFALNNA-----VKDAAKEHTDLNYV 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSSRNAASSSDVK----TKAATVTDTGGVDDKSFNQSAWEGLQAWGKEHNLSKDNGFTYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 PARK AVENUE
                                                                                                                  (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MORGAN & FINNEGAN, L.L.P
                                                                                                                                                  (212)
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ANTIGENIC PROTEINS AND
GENES ENCODING SAME OF BORRELIA BURGDORFERI.
                                                                                                                                                                                                              2026-4018US4
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US-08-396-957A-4
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; OTHER INFORMATION: p39a protein sequence
US-08-396-957A-5
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08396957A Patent No. 5780041
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
ANTIGENIC PROTEINS AND
ANTIGENIC PROTEINS AND
OF THE THE PROPERTY OF THE PROPER
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Best Local Similarity 26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 101;
                                                                                                                                                                        TITLE OF INVENTION: ANTIGENIC PROTEINS TITLE OF INVENTION: GENES ENCODING SAN NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: MORGAN & FINNEGAN, L.L.P. ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: p:
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 TKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 AGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASK--DKPSTLLAV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL TYPE:
                                               COUNTRY:
                                                                                  CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 ANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSSTAELEGKYSS-- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Borrelia burgdorferi
STRAIN: Sh-2-82
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVLERKIVNKEIIVP 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTIPAEEVRKTLEIP 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKNNNV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGLAGIGVIEAAKNLGDGYYVIGADQDQS--YLAPKN-FITSVIKNIGDALYLITGE-Y 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGYESGAKYAN-KDIEIISEYSNSFSDVDIG------RTIASKMYSKGIDVIHF 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A-----VVFRVEQGAFLAGYIAAKKSFSGK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDLDNLKRNGSDLIW-LVGYMLTDA--SLLVSSENPKI--SYGIIDPIYGDDVQIPENLI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSKKIKISMLV---DGVLDDKSFNSSANEALLRLKKDFPENIEEVFS--CAISGVYSSYV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGPLTEI-FSDIIANQND-RYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLY 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTGRYINLTYKTEEAGWLAGY--ANASFLAKKFPSDPTKRSAIVIG--GGISPAVTD-FI 208
                               10154
                                                                                                                                                  345 PARK AVENUE
                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                              GENES ENCODING SAME OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 178; DB 1;
Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 124; Indels
                                                                                                                                                                                                                                                                          BORRELIA BURGDORFERI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----IGFIGGMKGNIVDAFR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----EF-EYI 310
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                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                    08-396-957A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 07/48
APPLICATION NUMBER: 07/48
TITING DATE: 05-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,434
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: 07/664,731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
OTHER INFORMATION: p3
OTHER INFORMATION: se
                                                                                                                          93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Borrelia burgdorferi
STRAIN: Sh-2-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/0 FILING DATE: 19-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                   59 GTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYSSLANTNKNVWVLSG 114
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: p39'
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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YIGSFADLEAGRSVATRMYSDEID------IIHHAAGLGGIGAIEVAKELGSGHYI 238
                            KI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQ--NDRYL 286
                                                                                       YANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTD 232
                                                                                                                       FOHGD-AFTRWLKIPENKOLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAG 173
                                                                                                                                                                                      GTFDDKSFNESALNGVKKVKEEFKIELVLKESSSNSYLSDLEG----LKDAGSDLIWLIG
                                                              YIAAKL---
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01-MAR-1995
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                                                           -SKTGKIGFLGGIEGEIVDAFRYGYEAGAKYAN-----KDIKISTQ 188
                                                                                                                                                                                                                                                                                                                                              sequence.
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Patent No. 6248583
                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Chromosomally-Encoded Membrane TITLE OF INVENTION: Protein of Borrelia Burgdorferi NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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                    156 GRYINLIYKTEEAGWLAGYANASFLAKKFPSDPIKRSAIVIG---GGISPAVIDEIAGYL 212
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140 NS-LAIKFRNEEAAFLAGYIAAKMSRKE------KIGFLTGPMSEHLKDFKFGFK 187
                                                                                                    100 SSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGI----DWTDTENVIPT 155
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                                                                    92 EVQKNPLNLFWLI-GYRFSDL-----SVKLSYERPDIYYGIIDAFDYGDIQ--VPK 139
                                                                                                                                         34 VLAHGSFYDKGYNQSVHDGVVKLRDNFGIKLITKSLRPYPIEGKRLLTVDE--AMTEDAY 91
                                                                                                                                                                           55 VTAGGTVNDNSFNQSGWEAIQQLG-------ALTGGEITSVDSSTAELEGKY 99
                                                                                                                                                                                                              Match 6.6%;
Local Similarity 23.4%;
Les 83; Conservative 54
                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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Rochester
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30,727
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                                                                                                                                                                                                             Score 143; DB 4; I
Pred. No. 2.4e-05;
4; Mismatches 131;
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US-09-336-447A-15
; Sequence 15, App
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CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PACENTIN VET. 2.1
SEQ ID NO 15
LENGTH: 889
TYPE: PRT
ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.4%; Score 137.5; DB 4; Best Local Similarity 22.8%; Pred. No. 0.00036; Matches 112; Conservative 78; Mismatches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 15, Application US/09336447A
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APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
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APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
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   612
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                                                                                                                                                                                                                                                        VTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTL 263
KOTEATDALNKASSENTONI -- EDLAAYNELODAYAKOOTEATDALNKASSENTONIAKN
                                    --TEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQPDKQQESLDK-------
                                                                                                           YTKKSN-SRNLAGFEFGKKSATVYLG--IKDRFVDIADTSLEGNDKKLA--
                                                                                                                                                                               LAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDL
                                                                                                                                                                                                                                                                                                                                                                   GIDNKANADNAVALGNKNTIEGENSVAIGSNNTVKKNQKNVFILGSN-TDTKDA-QSGSV 384
                                                                      IDQKADLTKDIKALESNVEEGLLDLSGRLIDQKADIAQN--QANIQDLAAYNELQDQYAQ
                                                                                                                                             LNLSGRLIDQKADIDNNINHIYELAQQQDQHSSDIKT-----LKKNVEEGLLELSGHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GGEQNQAIGKYSTISGGRQNEASGDRSTVAGGEQNQAIGKYSTVSGGYRNQATGKGSFAA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GWEAIQQLG---ALTGG--EITSVDSSTA-----ELEGKYSSLA------
                                                                                                                                                                                                                      STDAVNGSQLYALAAAVDDNQYDIEKNQDDIAKNQADIAKNQADIQTLENDVGKE----L
                                                                                                                                                                                                                                                                                              {\tt LLGDNTSGKAATAVEDATVGDLSLTGFAGVSKANSGTVSVGSEGKERQIVHVGAGRISND}
                                                                                                                                                                                                                                                                                                                   I---NLTYKTEEA-------GWLAGYANASFLAKKFPSDPTKRSAIVIGGG-ISPA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKSNSRNLAGFEFGKKSATVYLGIKDRFVDIA-DTSLEGNDKKLATEAISEAKK 378
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APPLICANT: DRUILHE, PIERRE
APPLICANT: DAUBERSIES, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAFILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1998-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER APPLICATION NUMBER: FR 95/07007
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 8
LENGTH: 1786
RESULT 7
US-09-308-375-2
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Best Local :
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OTHER INFORMATION: Description of Artificial Sequence:Polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                             232 DKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIF---SDIIANQNDRYLIG
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                                                                                                                                                                        LTDKMIDAVEESIEISSDSKEETESIKDKEKDVSLVVEEVQDNDMDESVEKVLELKNM--
                                                                                                                                                                                                   IKDREVDIADTSLE-GNDKKLATEAISEAKKE----FEEKTKTIPAEEVRKTLEIPEMPD 403
                                                                                                                                                                                                                                                                                                         VDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLG 348
                                                                                                                                                                                                                                                                                                                                                     EHVEQNVYVDV------DVPAMKDQFLGILNEAGGLKEMFFNLEDVFKSESD--VIT 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDAFTRWLKIPENKOLFTEKNIIILGIDWTDTENVIPTGRY----INLTYKTEEAGWLAG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVNDNSF---NQSGWEAIQQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLSGFQH 117
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                                                                                        -----EEELMKDAVEINDI 1239
                                                                                                                                 KQPDKQQESLDKLITDINNL 423
                                                                                                                                                                                                                                                                VEEIKDEPVQKEVEKETVSIIEEMEENIVDVLEE---EKED
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Sequence 2, Application US/09308375 Patent No. 6300117

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TITLE OF INVENTION: Proteases From Gram-Positive Organisms
FILE REFERENCE: GC394-PCT
CURRENT APPLICATION NUMBER: US/09/308,375
CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 2285
TYPE: PAT
ORGANISM: Bacillius subtilis
US-09-308-375-2
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: Sequence 2, Application US/08409995

: Patent No. 5646259
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                                      PATENI NO. JANUARY GENERAL INFORMATION:
APPLICANY: Barenkamp, Stephen I.
APPLICANY: St. Geme III, Joseph W.
APPLICANY: St. Geme III, Joseph W.
TITLE OF INVENTION: Haemophilus Adhesion Proteins
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & He
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Best Local Similarity
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                     STATE:
COUNTRY:
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USA
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                                                                              Albritton & Herbert
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TELEFAX: (415) 388-3249;
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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                                                                                 734
                                                                                                                                                                                                                                                                                     228 KITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQND-RYL
                                                                                                                                                                                                                                                                                                                                                                                        208
                                                                                                                                                                                                                                                                                                                                                                                                                                 527 TYSLQDAL-----TGLTSITLGTGNNGAKTEINKDGLTITPANGAGANNANTISV 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 TEDADEGKGLVTAKDVI--DAVNKTGWRIKTTDANGQNGDFATVASGTNVTFASGNGTTA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   289 TVEFLSADTETTTVTVDSKENGKRTEVKIGAKTSVIKEKDGKLFTGKANKETNKVDGANA 348
794
                                                                                                                         324 YTKKSNSRNLAG---FEFGKKSATVYLGIKDRFVDIADTS------LEGN----
                                                                                                                                                                    683 SGNGINVSGKTVNGRREITFELAKGEVVKSNEFTVKETNGKETSLVK------VGDK 733
                                                                                                                                                                                                                                                                                                                                             577 TKDGISAGGQSVKNVVSGLKKFGDANFDPLTSSADNLTKQNDDAYKGLTNLDEKGTDKQT 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 LAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 -----MAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYS 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFTEKNII--ILGIDWTDT------ENVIPTGRYI-----NLTYKTEEAGW 170
                        -----DKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDK 404
                                                                                                                                                                                                                                                        PVVADNTAATVG-DLRG------LGWVISADK-----TTGGSTE-YHDQVRNANEVKFK 682
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IAKSGFELGLADEA -- DAKRAFDDKTKALSA -- -- GTTEIVNAHDK 833
                                                                                   YYSKEDIDLTTGQPKLKDGNTVAAKYQDKGGKVVSVTDNTEATITNKGSGYVTGNQVADA
                                                                                                                                                                                                               IG-----TSILKNLGYSVFSVLSDL
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st Local Similarity
tches 112; Conserv
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
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PRIOR APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: S11va, Robin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 6
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577 TKDGISAGGQSVKNVVSGLKKFGDANFDPLTSSADNLTKQNDDAYKGLTNLDEKGTDKQT
                                                                                                                                                           467
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TOPOLOGY: unl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States ZIP: 94111-4187
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                                                                                                               LAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDF----
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                                                                           TYSLQDAL-----TGLTSITLGTGNNGAKTEINKDGLTITPANGAGANNANTISV
                                                                                                                                                                                                                                                                     SLANTNKNVWVLSGFQHGD-------AFTRWLKI-------PENKQ 132
                                                                                                                                                     LVTAKGLVTALNSLSWTTTAAEADGGTLDGNASEQEVKAGDKVTFKAGKNLKVKQEGANF 526
                                                                                                                                                                                           LFTEKNII -- ILGIDWTDT------ENVIPTGRYI-----NLTYKTEEAGW 170
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                                       -----IAGYLAGIKAW-----
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Four Embarcadero Center, Suite 3400
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Pred. No. 0.04;
5; Mismatches 170;
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; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-377-155-32
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US-09-377-155-32
; Sequence 32, A
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Patent No. 6197312
GENERAL INFORMATION:
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Best Local
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NUMBER OF SEC. 1997-12-12
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
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PVVADNTAATVG-DLRG-----LGWVISADK-----TTGGSTE-YHDQVRNANEVKFK
                                 KITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQND-RYL
                                                                      {\tt TKDGISAGGQSVKNVVSGLKKFGDANFDPLTSSADNLTKQNDDAYKGLTNLDEKGTDKQT\\
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                                                                                                                                                                                                                          LVTAKGLVTALNSLSWTTTAAEADGGTLDGNASEQEVKAGDKVTFKAGKNLKVKQEGANF
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JENNINGS, Michael Paul
MOXON, E. Richard
WENTION: NOVEL SURFACE ANTIGEN
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19.1%; Pred. No. 0.04;
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                                                                                                                    Matches
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CITY: San Francisco
STATE: California
Tnited Stat
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APPLICATION NUMBER: US 08/409,995
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barenkamp, Stephen J.
TITLE OF INVENTION: HAEMOPHILUS ADHESION PROTEINS
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   NAME: VANCE, DOLLY A.
REGISTRATION NUMBER: 39,054
REFERENCE, DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US96/4031 FILING DATE: 22-MAR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hohbach Test Albritton & Herbert
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                                                                                                                                                                                                                                                                                                                          TELEFAX: 1-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 29-DEC
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                                                                                                                                   Local
                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                 7 TKEEKSADNQNKQITDVSKISG-----
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------MAIVTAGGTVNDNSENQSGWEAIQQLGALTGGEITSVDS;T----AELEGKYS 100
                                                  TVEFLSADTETTTVTVDSKENGKRTEVKIGAKTSVIKEKDGKLFTGKANKETNKVDGANA 348
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29-DEC-1997
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7 TKEEKSADNQNKQITDVSKISG------LVNERKSEIMAAKA--DANKHEGLN-

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TVEFLSADTETTTVTVDSKENGKRTEVKIGAKTSVIKEKDGKLFTGKANKETNKVDGANA 348

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TEDADEGKGLVTAKDVI--DAVNKTGWRIKTTDANGQNGDFATVASGTNVTFASGNGTTA 406

-----MAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGEITSVDSST----AELEGKYS 100

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PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR PLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 32
FENOTH: 1098
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                                                                                                          ; ORGANISM: Haemophilus influenzae US-09-669-974-32
  Query Match
Best Local Similarity
Matches 112; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 32, Application US/09669974 Patent No. 6333173
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CURRENT FILING DATE: 2000-09-26
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
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                      5.5%;
Score 117.5; DB 4;
Pred. No. 0.04;
75; Mismatches 170;
                                          Length 1098;
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APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
                                                                                                                                                                                                                                                                                 Query Match 5.5%;
Best Local Similarity 19.1%;
Matches 112; Conservative 75
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                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PATENTIN Ver. 2.0
RO ID NO 44
LENGTH: 1098
TYPE: PRT
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                                 LFTEKNII--ILGIDWTDT------ENVIPTGRYI-----NLTYKTEEAGW 170
                                                                                                     SLANTNKNVWVLSGFQHGD-----AFTRWLKI-----
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LVTAKGLVTALNSLSWTTTAAEADGGTLDGNASEQEVKAGDKVTFKAGKNLKVKQEGANF
                                                                  TVTNGTDGITVKYDAKVGDGLKLDGDKIAADTTALTVNDGKNANNPKGKVADVASTDEKK 466
                                                                                                                                       TEDADEGKGLYTAKDVI--DAVNKTGWRIKTTDANGQNGDFATVASGTNVTFASGNGTTA 406
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                                                                                                                                                                                                                                                                                                  Score 117.5; D
Pred. No. 0.04;
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-923-992A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08923992A Patent No. 6280738 GENERAL INFORMATION:
                                                                                                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
                                                                                                                        TELEFAX: (202) 371-250 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA FC
TITLE OF INVENTION: Streptococcal Beta
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,992A
                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino aci
                                                                                                                                                               REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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ZIP: 200
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                                                                                                                                                                                                                            NAME: Esmond, Robert W. REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                             amino acid
                                                                                1104 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-1997
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Best Local Similarity Matches 85; Conserv

Conservative

78;

Mismatches

5.4%; Score 116.5; DE 17.9%; Pred. No. 0.051;

DB 4; 208;

Length 1104; Indels

103;

Gaps

13;

Query Match

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10

EKSADNQNKQITDVSKISGLVNERKSEIMAAKADANKHFGLNMAIV?AGGTVNDNSFNQS

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RESULT 15
US-09-074-658-75
; Sequence 75, Application US/09074658
; Patent No. 6184371
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                                                       TELEFAX: (416) 595-11
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                          REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN
NUMBER OF SEQUENCES: 78
                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 SAQQELEKLEKAI -- KELMEQPEIPSNPEYGIQKSIWESQKEPIQEAITSFNKI 594
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                                                                                                                                                 NAME: Stewart, Michael I REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 08-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: Canada
ZIP: M5G 1R7
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                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E----NKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKF 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVKVREELGKLFSSTKAGLDQQIQEHVKKETSSEENTQ------KVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQPDK-----QQESLDKLITDINNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Toronto
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h Floor, 330 University Avenue
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acid
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Best Local 9
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                                                                        541 ----ASKAVSRPEQLSHNAARISE-FSDYADDGKYKYLLGK----
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                                                                                                                                                                                                                            432 FIDEHHRRRRMGLLYRYENEAYSDNWADKAVLSFDKQGVATDNNTLKLNCAVYPSVDK--
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                                                                                                                                                                                                                                                                                                                                                                                  316 A-RHENLSAQAYTGGGRILPDPMDYRSGSWLAKLGYRFGGRHYVGGVFEDTKQ----RYDI 371
580 VEG---SVCGYIETLRSRKCVPRKING-----SNIHISLNDRF
                                  309 LKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF
                                                                                                                                                                                      209 AGYLAGIKAWNLKNSDK---------KTKITTDKIEINLGFDVQDTSTKER 250
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                                                                                                                                                                                                                                                                                                                                            102 LANTNKNVWVL------SGFQHGDAFTRWLK-IPENKQLFTEKNIII-LGIDWTDTE 150
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                                                                                                                                                                                                                                                                                                                                                                                                                    44 ANKHFGLNMAIVTAGGTVNDNSFNQSGWEAIQQLGALTGGE--ITSVDSSTAELEGKYSS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 KETTKEEKSADNQNKQITDVSKISG-----LVNERK-----SEIMAAKAD
                                                                                                              LEQIASK--DKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSI 308
                                                                                                                                                    ACRASADKPYSYDSSDRFHYREQHNVLNALFEKSLKNKWTKHHLTLGFGYD-
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78; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 113.5; DB 4; Pred. No. 0.075;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158;
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Search completed: July 18, 2002, 09:14:57 Job time: 37 sec

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           Mycoplasma hyopneu
Mycoplasma hyopneu
43kd regression as
Cancer metastasis
Gene encoding the
Inflammatory cytok
Membrane protein M
Streptococcus pneu
Streptococcus facca
Enterococcus facca
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6 16 AAR75739 B	114 5.0 1333 22 AAU35343	114.5 5.0 1166 20 AAY08643	115.5 5.0 1164 21 AAY84459	115.5 5.0 1164 19 AAW40537	115.5 5.0 1164 17 AAR85781	116 5.0 1300 22 AAU35313	116 5.0 1300 22 AAU33407	116.5 5.1 873 19 AAW68207 M.	117 5.1 2353 17 AAR99393	5 117.5 5.1 1079 21 AAB01836	4 117.5 5.1 1073 21 AAB01837	3 119 5.2 892 19 AAW68203	2 119 5.2 776 22 ABB52597	1 120 5.2 719 22 AAG79241	0 121.5 5.3 1099 19 AAW40538	9 121.5 5.3 834 21 AAY93404	8 122 5.3 2411 21 AAB23860	7 122.5 5.3 2346 22 ABB63519	6 122.5 5.3 2285 20 AAW98149	5 124.5 · 5.4 1135 21 AAY84460	4 129 5.6 441 18 AAW28236	3 129.5 5.6 1558 21 AAB18324	2 131.5 5.7 1786 18 AAW24790	1 141.5 6.2 889 19 AAW68208	0 144 6.3 353 22 AAE03741	9 150 6.5 223 21 AAY91298 Gro	8 162 7.0 339 20 AAY19984 B.	7 162 7.0 339 19 AAW61757 B.	6 162 7.0 322 20 AAY19985 B.	5 165.5 7.2 340 14 AAR31013	172 7.5 341 14 AAR33280	173 7.5 166 22 AAU07352 Int		Inter p39-e p39-e B. bu B. ch	AAU07352 AAR31013 AAR31013 AAR31013 AAR19985 AAW19984 AAW19984 AAW19984 AAW21998 AAW24790 AAB18324 AAW28236 AAW28236 AAW28236 AAW38360 AAW38360 AAW38360 AAW393404 AAW68203 AAW68203 AAW68203 AAW68207 AAW35313 AAW68207 AAU333407 AAU35313 AAW40537	144 144 120 120 120 121 121 121 121 121 121 121	146 340 340 340 332 339 339 339 339 1786 1558 1413 1558 2241 1135 2241 1073 1073 1107 1107 1107 11164 11164 11164	45555555555555555555555555555555555555	173 165.5 162 162 163 164 141.4 141.5 129.	4444443333333333222221111113 4444443333333332222221111113
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Misc-difference 152
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                           Misc-difference
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                                                                                                            Mycoplasma hyopneumoniae
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MHP3; antigen; vaccine; enzootic mycoplasma pneumonia; antibody; immunoassay; immunotherapy; anti-idiotypic antibody.

07-SEP-2001 AAU01859;

(first entry)

Mycoplasma hyopneumoniae MHP3 antigen.

AAU01859 standard; Protein;

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Best Local Similarity
Matches 451; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence is Mycoplasma hyopneumoniae MHP3 antigen. MHP3 antigen and its fragments are useful in manufacturing a vaccine for treating c preventing a disease or disorder in an animal, especially pig, caused by M. hyopneumoniae infection e.g. enzoctic mycoplasma pneumonia. The mhp3-encoded proteins may be used as immunogens to generate antibodies which immunospecifically bind such an immunogen. The antibodies generated against the antigen are useful in diagnostic immunoassays, passive immunotherapy and generation of anti-idiotypic antibodies. Mhp3 proteins may also be used in immunoassays, e.g. to detect or measure in a biological sample from a vaccinated or potentially infected test animal the presence of antibodies to the antigen, and thus to monitor the immune response and/or to diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New apoprotein antigens ehooded by mhp3 gene from Mycoplasma hyopneumoniae useful as a vaccine for treating or preventing diseases caused by Mycoplasma hyopneumoniae -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection
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AGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTE
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                                                               LAGFEFGKKSATYYLGIKDRFYDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEV
                                                                                                                                                                                                       RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSST 120
                                                   lagfefgkksatvylgikdrfvdiadtslegndkklateaiseakkefeektktipaeev
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DB; AAS03285.
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Pred. No. 5.2e-165;
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                                                                                                                                 Query Match 91.7%;
Best Local Similarity 99.8%;
Matches 414; Conservative
                                                                                                                                                                                                                            The sequence represents Mycoplasma hyopneumoniae a recombinant MHP3 antigen lacking the first 28 amino acids (the putative signal sequence). MHP3 antigen and its fragments are useful in manufacturing a vaccine for treating or preventing a disease or disorder in an animal, especially pig, caused by M. hyopneumoniae infection e.g. enzootic mycoplasma pneumonia. The mhp3-encoded proteins may be used as immunogens to generate antibodies which immunospecifically bind such an immunogen. The antibodies generated against the antigen are useful in diagnostic immunoassays, passive immunotherapy and generation of anti-idiotypic antibodies. Mhp3 proteins may also be used in immunoassays, e.g. to detect or measure in a biological sample from a vaccinated or potentially infected test animal the presence of antibodies to the antigen, and thus to monitor the immune response and/or to diagnose
                                                                                                                                                                                                                                                                                                                                                                                                                          New apoprotein antigens encoded by mhp3 gene from Mycoplasma hyopneumoniae useful as a vaccine for treating or preventing caused by Mycoplasma hyopneumoniae -
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                                                                                                                                                                                                                    antigen, and infection of
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TRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLA
                                 2001-309781/33.
DB; AAS03286.
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Pred. No. 9.9e-151;
0; Mismatches 1;
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16-SEP-1987;
11-DEC-1987;
04-JAN-1988;
16-MAR-1990;
02-OCT-1992;
                is used to of tumours
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 Disclosure;
                     DNA encoding a regression-associated antigen from M. is used to obtain prods. for diagnosis, localisation
                                                                                                                                                               07-SEP-1993
                                                                                                                                                                            US5242823-A
                                                                                                                                                                                                        Misc-difference
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                                            N-PSDB;
                                                                                (ITGE-)
                                                                                                                                               07-MAR-1986
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                                                                                                                                                                                                                                                                                                                     Regression
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DB; AAQ47816.
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                                                                                                                                                                                                                                                                                                                     associated antigen;
Figure 3;
                                                                  Ghosh-dastidar
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870S-
870S-
880S-
900S-
920S-
                                                                                                                                                                                                                                                                                                            antibodies; antibodies;
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/note=
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English
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Regression associated antigens (RAA's) are identified in material from neoplastic cells by their immunolyical reactivity with regression associated antibodies from the serum of patients diagnosed as undergoing regression of a tumour. RAA's can be used.
              Misc-difference
                                      Misc-difference
                                                                 Misc-difference
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                                                                                                                               Homo
                                                                                                                                                         Cancer metastasis;
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                                                                                                                                                                                                                                    AAR67582;
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                                                                                                                               sapiens
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              /note= "corresponding
319
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88; Mismatches 150;
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Best Local Similarity
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          AAP93343
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                                                                                                            YLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEM---P
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                                                                                                                                   ykgisddfvgvsnstvadadkvkaqeflneatadfkkqiqanpt-nyksvlgiptmlind
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DB; AAQ79124.
         standard;
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illarity 39.0%;
Conservative 8:
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Pred. No. 4e-44;
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Best Local
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Peptide
Protein
                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ITGE-) INT
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svvdaikksnkdtkyligvdtdqskifppa-tvfft-iekhlgrtiyevitdiwlkked
                                                            LAGIKAMNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLT
                                                                                                                                                                                                      NKHFGLNMAIVTAGGTVNDNSFNQSSWEAI----QQLGALTG-GEITSVDSSTAELEGKY 127
                        EIFSDII--ANQNDRYLIGVDTDQSLYYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSN
                                                                                                                                           knflngnknvwiltgfqqgqefpkflkqtdsngkkysdllaekkvilvavdwdlskedkd
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                                                                                                                                                                                         -knfdfntvlltaggtvqdksfnqsiweavlehydqiekttnldrvsqetnnqseligky 113
                                               lagiakynndnptakvtisdnninidtgf-isndftatfingivnks--slvlpvvgslt
                                                                                                                                                                                                                                                                                        tch 28.5%; Score 655; DB 10; al Similarity 37.4%; Pred. No. 4e-41; 171; Conservative 89; Mismatches 149;
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                                                                                                                                                                                                                                                                                                               Length 448;
                                                                                                                                                                                                                                                                                        Indels 48;
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                                                                                                                                                                                                                                                                                                                                                                                    monospecific
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                                                                                                                                                                                                                               Query Match
est Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                             This sequence represents the inflammatory cytokine of the invention. The inflammatory cytokine can be used in a drug, which useful for the treatment of thrombocytopaenia.
                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                              New inflammatory cytokine inducer gene treatment of thrombocytopaenia
                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX33847.
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-281057/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inflammatory cytokine inducer.
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                                                                                                                                                                                KAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS------KDKPSTLL
                                                                 GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGI 243
                                                                                                             EGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT
                                                                                                                                   EIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAEL 123
                                                                                                                                                                                                       IKWNKFLGLGLVFPLSAI-ATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKS 63
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lyynqkh--ksskiyhtspvkldsgf-----tagekmntvinnvlsstpadvkynphvil
                                         --fyslqfnikesafttgyalaswlseq---deskrvvasfgggafpgvttfnegfakgi
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                                                                                                                                                                                                                                                                                        428
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytokine inducer; thrombocytopaenia; therapy
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                                                                                                                                                                                                                             17.2%; Score 394.5; DB 20; 26.8%; Pred. No. 1.6e-21; Live 101; Mismatches 174;
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                                          Query Match
Best Local Similarity
Matches 127; Conserv
                                                                                                                   This sequence is a membrane protein designated M161Ag. Oligonucleotide probes for the cDNA were designed from putative N-terminal M161Ag peptide sequences isolated from P93 cells. M161Ag can be used in the development of a leukaemia treating agent.
                                                                                               Sequence
                                                                                                                                                                                             Membrane protein M161Ag treating agent
                                                                                                                                                                                                                              N-PSDB; AAT75133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW22727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW22727 standard;
                                                                                                                                                                     Claim 1; Fig 1; 6pp; Japanese.
                                                                                                                                                                                                                                        WPI; 1997-369470/34.
                                                                                                                                                                                                                                                            (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                   05-DEC-1995;
                                                                                                                                                                                                                                                                                                       05-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M161Ag; membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Membrane protein M161Ag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    402 SEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDINK 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293
            5 IKWNKFLGLGLVFPLSAI-ATISAGCWDKETTKEEKSADNQNKQIT----DVSKISGLVN 59
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mkkskkillgl-spiaailpavavsc----
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                                                                                               429
                                           Conservative
                                                                                               AΑ;
                                                                                                                                                                                                                                                                                  95JP-0344504.
                                                                                                                                                                                                                                                                                                      95JP-0344504
                                                                                                                                                                                                                                                                                                                                                                                                      /note= "selenocysteine"
348
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "selenocysteine"
185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; leukaemia; treatment.
                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                          /note= "selenocysteine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "selenocysteine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                     16.9%;
                                                                                                                                                                                                                                                                                                                                                                     "selenocysteine"
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                                                                                                                                                                                                       useful in development of leukaemia
                                        96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             429
                                        Score 387.5; DB 18;
Pred. No. 5.4e-21;
6; Mismatches 174;
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                                          Indels
                                                               Length 429;
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specifically claimed nucleotide sequences isolated from S. pneumoniae. The sequences have antibacterial and antiinflammatory properties. The protein sequences, and fragments of them, are useful as immunogens and/or antigens. The nucleotide sequences can be used in vaccines and diagnostic assays. The proteins and nucleotides can be useful for the
                                                                      AAY81501
isolated
                                                                                                                                          New Streptococcal protein, useful as a vaccine, pneumococcal diseases and for screening agents cor inhibiting expression of the protein -
                                                                                                                                                                                                                                Gilbert CFG,
                                                                                                                                                                                                                                                                                                                                                                                      WO200006737-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus
                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                        27-JUL-1998;
19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                             10-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae; vaccine; screening; protein antigen; antibacterial; antilnflammatory; meningitis; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY81632 standard; Protein; 351
                                                                                                                                                                                                                                                                                                                                 27-JUL-1999;
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                                                                                                                                                                                                                                                            (MICR-) MICROBIAL TECHNICS
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                                                                      to AAY81679 represent specifically claimed protein sequences from Streptococcus pneumoniae. AAA05407 to AAA05590 represent
                                                                                                                Page 85; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                Hansbro
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99US-0125164.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection and diagnosis of S. pneumoniae. The protein sequences are also useful for screening an agent capable of antagonising, inhibiting or interfering with the function or expression of the proteins in which the agent is useful for treatment or prophylaxis of S. pneumoniae infection and meningitis. AAAO5591 to AAAO5614 represent primers used in the
                                                  31-OCT-1996;
                                                                                                                                                                                                                        Streptococcus pneumoniae SP007
                                                                                                                                                                                                                                                                                                    AAW55066 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                        (HUMA-) HUMAN GENOME SCI INC
                                                                            30-OCT-1997;
                                                                                                      07-MAY-1998
                                                                                                                               WO9818930-A2
                                                                                                                                                         Streptococcus
                                                                                                                                                                                   detection;
                                                                                                                                                                                               Streptococcus pneumoniae;
                                                                                                                                                                                                                                                   02-OCT-1998
                                                                                                                                                                                                                                                                             AAW55066;
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                                                                                                                                                                                                                                                                                                                                                                                              KKLATEAISEAKKEFEEKTKTIPAEE 419
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-avedakakildgsvkvpekz
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                                                                                                                                                                                 pneumonia;
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                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                         pneumoniae.
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                                                                                                                                                                                 antigen; vaccine; infection; tis media; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                       -snkaergefpggq---vivyslkdkgvdlavtnlseeg
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Pred. No. 5.1e-09;
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                                                                                                                                                                                              diagnosis;
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GH,

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in protective or therapeutic vaccines, and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
Enterococcus faecalis; 
detection; attenuation;
                                                   Enterococcus
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                                                                                     20-APR-1999
                                                                                                                                                       AAY00049 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                              --ivyqvaggtgagvfaeakslnesrpenekvwvigvdrdqeaegkytskdgkesnfvlv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDK
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-avedakakildgsvkvp
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                 faecalis;
                                                 faecalis antigenic polypeptide fragment EF021.
                                                                                   (first entry)
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               infection; vaccine;
 antigenic
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Pred. No. 3
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                 immune response; diagnosis;
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Matches 104
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The unclectide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for secreening compounds to identify agonists and antagonists of E. faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an antigenic polypeptide fragment isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-070095/06
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                                  VDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD
                                                                                                                                                          kgkalaaamyqngvdiifhasgatgqgvfqeakdlnesgsgdkvwvigvdrdqdadgky-
                                                                                                                                                                                                                                           vvidrfqagfekgv-adaakelgkeitvdt---
                                                                                                                                                                                                                                                                                                                                                                                                           iqsndaadyttnidqavsskfntifgi----gyllkda-----issaadanpdtnfvli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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97US-0044031.
97US-0046655.
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 182; DB 20;
Pred. No. 1.2e-05;
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AAY00048
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                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 104
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06-MAY-1997;
16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a protein isolated from Enterococcus faecalis. The present invention describes genes, proteins and antigenic polypeptides isolated from E. faecalis. The proteins can be used in vaccines for preventing or attenuating an infection caused by a member of the Enterococcus genus in an animal. They can also be used for detecting Enterococcus antibodies in a sample. The nucleotide sequences can be used for detecting Enterococcus nucleic acids. Products from the present invention can also be used for screening
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Enterococcus faecalis polynucleotides - used products for the detection of Enterococcus and for use in for prevention or attenuation of Enterococcus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY00048 standard;
                                                                                                                                                                                                                                                                                                                               activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
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                                                                                                                                                                                                            61 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGA---LTGGE----
                                                                                         GIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISP
                                                                                                                                                                                  ktaesgggkgda----ahsaviitdtggvddksfnqssweglqawgkehdlpegskgyay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-070095/06
DB; AAX20038.
 TLLAVAGPLTEIFSDII--
                                                  AVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPS
                                                                              ddqidgkknv-----vsatfrdneaaylagvaaa---
                         vvidrfqagfekgv-adaakelgkeitvdt------
                                                                                                                                                       ITSVDSS--TAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIIL 170
                                                                                                                               iqsndaadyttnidqavsskfntifgi----gyllkda-----issaadanpdtnfvli 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
                                                                                                                                                                                                                                    h 7.9%;
Similarity 25.4%;
04; Conservative !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 100;
                                                                                                                                                                                                                                                                                                                                          to identify agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    attenuation;
                                                                                                                                                                                                                                                                                                     361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  faecalis;
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97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection; vaccine; immune response; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                    Score 182; DB
Pred. No. 1.3e<sup>o</sup>
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EF021
                                                                                                                                                                                                                                                                                                                                           and antagonists of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunsch CA;
                                                                                                                                                                                                                                      DB 20;
..3e-05;
les 139;
 ANQUDR-YLIGVDTDQSL--VYT
                                                                             ----netktnkvgfvggeeg 179
                                                                                                                                                                                                                                                             Length 361;
                                                                                                                                                                                                                                                                                                                                             (F)
                                                                                                                                                                                                                                      Indels 116;
                                                                                                                                                                                                                                                                                                                                          faecalis protein
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                                                                               Best Loc
Matches
                                                                                                   Query Match
                                                                                                                                                                                  The antigenic protein p39 alpha is immunoreactive with mammalian Lyme borreliosis serum. The Borrelia antigenic proteins p39 alpha and p39 beta are used in vaccines to protect against Lyme disease, as assay reagents to detect specific antibodies in the serum (diagnostic of Ly disease), and to raise antibodies, either for diagnosis (by detecting
                                                                                                                                                                          the
                                                                                                                                                                                                                                                                 Example 6; Columns 31-34; 33pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                     19-FEB-1993;
01-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5780041-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borrelia burgdorferi; antigenic protein; p39
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                                                                                                                                       Sequence
                                                                                                                                                              expression
                                                                                                                                                                                                                                            This represents the Borrelia burgdorferi antigenic protein p39 beta
                                                                                                                                                                                                                                                                                                   New antigenic for raising
                                                                                                                                                                                                                                                                                                                                                                         Schwan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUL-1998
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                                                                               Local Sir
hes 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     burgdorferi antigenic protein
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                                                                                                                                                              corresponding ression of the
             --LANTNKN---
                                sskkikismlv---dgvlddksfnssaneallrlkkdfpenieevfs--caisgvyssyv
                                              ANKHFGLNMAIYTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAELEGKYSS--
                                                                                                                                                                                                                                                                                                                                                 1998-413001/35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     borreliosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTK-----NKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF
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                                                                                                                                                                                                                                                                                                                                                                         TG,
                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                      AAV35685,
                                                                                                                                        341
                                                                                                                                                                                                                                                                                                                                                                                              DEPT HEALTH & HUMAN SERVICES
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                         Simpson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                   proteins from antibodies or
                                                                                                                                                                                                                                                                                                                                                                                                                   91US-0664731.
90US-0487716.
93US-0020245.
95US-0396957.
                                                                                                                                        Ā
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-VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lyme
                                                                                                                                                                         antigen) or in screening agents for ability to inhibit
                                                                                                                                                                                                                                                                                                                                       AAV35687
                                                                                                                                                               proteins
                                                                                                                                                                                                                                                                                                                                                                          ¥
                                                                                         7.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease.
                                                                             Score 179; DB
Pred. No. 2e-0
59; Mismatches
                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341
                                                                                                                                                                                                                                                                                                    Borrelia burgdorferi useful in vaccines for diagnostic detection of specific
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                                                                                         2e-05;
                                                                                                    DB 19;
                                                                                123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha; p39 beta;
                                                                                                    Length 341;
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                92;
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           181
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                       The invention relates to a novel secreted autostimulatory factor, interleukin-X (II-X), from an Epstein Barr virus (EBV)-carrying lymphoblastoid cell line. IL-X proteins can be used to enhance the growth of cells in vitro, or to grow primary human B cell cultures to facilitate
                                                                                                                                                                                                  New IL-x polypeptides useful e.g. for enhancing the growth of cells vitro, for growing primary human B cell cultures to facilitate proliferation of these cell lines, as therapeutics or prophylactics, molecular weight standards
                                                                                                                                                                                                                                                                                                                                                                                                          Blazar BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-AUG-1994;
11-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2001; 2001US-0760541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-2002
proliferation
                                                                                                                                                   Claim 1; Page 7; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2001019713-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WEBB/)
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)B; AAS11798.
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WEBB A C.
                                                                                                                                                                                                                                                                                                                                                                                                          Webb AC;
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; B cell.
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93US-0026132
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or prophylactics,
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Best Local S
Matches 50
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                                                                                                                                                                                                                                                                                                                                                  Polymerase chain reaction; PCR; primer; open reading frame; ORF; antigen; 39-alpha; 39-beta; serum; human; Lyme patient; p39-beta; p39-alpha; promoter; -10; -35; ribosomal binding site; RBS.
                                                                        New Borrelia burgdorferi protein and DNA isolates detection of Lyme borreliosis infection and in proantibodies and vaccines
                                                                                                                                                                                                                                              05-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                        P39-beta
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11-MAY-1993
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                                                                                                                                                                                                                       05-MAR-1990;
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                                                                                                                                                                                                                                                                                                                          Borrelia burgdorferi.
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                                                Disclosure; Page 36-39; 69pp; English.
                                                                                                                             N-PSDB; AAQ34672.
                                                                                                                                         WPI; 1993-017799/02.
                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN
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Local Similarity 27.3%;
ses 50; Conservative 3
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                                                                                                                                                                    Simpson
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(first entry)
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Pred. No. 2.1e-05;
7; Mismatches 56;
                                                                                                                                                                                              SERVICE
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rodn. of
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The sequences given in AAR31013 and AAR33280 represent the burgdorferi proteins P39-alpha and P39-beta. The DNA encoc proteins was isolated by polymerase chain reaction (PCR) us

(PCR) using encoding

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Canculated patent numbers. For further information please wish the Derwent can be protein the patent number format of the patent number format of the patent number of patent can be protein to be prevent can be protein the patent number of the patent number of
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Matches 100
                                                                     Polymerase chain reaction; PCR; primer; open reading frame; ORF; antigen; 39-alpha; 39-beta; serum; human; Lyme patient; p39-beta; p39-alpha; promoter; -10; -35; ribosomal binding site; RBS.
                         Borrelia burgdorferi
                                                                                                                                                                                    P39-alpha
                                                                                                                                                                                                                                         17-DEC-2001
11-MAY-1993
                                                                                                                                                                                                                                                                                                                          AAR31013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               site at www.derwent.com/dwpi/updates/ntis_us.html.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ygyesgakyan-kdieiiseysnsfsdvdig-----rtiaskmyskgidvihf 221
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26.7%;
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Pred. No. 6.8e-05;
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cc primer sequences given in AAQ34673-76. This DNA contained two open creading frames (ORF). It was therefore concluded that the P39 antigen which has been previously described is not one protein but two, 39-alpha cand 39-beta. The P39 signal appears to be enhanced when both genes calculated molecular weight of 36.926 kD. The protein with a calculated molecular weight of 36.926 kD. The protein encoded by this calculated molecular weight of 36.926 kD. The protein encoded by this calculated in the serum from human Lyme patients. The ORF conclectides downstream of p39-beta. This genes' ORF starts 116 conclectides downstream of p39-alpha and encodes a protein of 341 amino calculated in the promoter located 5' of p39-alpha appears to be present with classic -10 and -35 regions whereas p39-beta lacks a crecognisable promoter sequence. Both genes have putative ribosomal control of the promoter sequence. Both genes have putative ribosomal control of the patent of the genes shave 628 similarity.

CC (Note: Revised entry submitted to correct the patent number format of CC us Government-owned NTIS applications to prevent classes with ongoing US granted patent numbers. For further information please visit the Derwent com/dwpi/updates/ntis_us.html.)
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Borrelia burgdorferi protein and DNA isolates - used detection of Lyme borreliosis infection and in prodn. of antibodies and vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in AAR31013 and AAR33280 represent the B. burgdorferi proteins P39-alpha and P39-beta. The DNA encodin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-017799/02.
N-PSDB; AAQ34672.
                                                                                                                                                                                                                                                                                                                                                                                                                             proteins was isolated by polymerase chain reaction (PCR) using primer sequences given in AAQ34673-76. This DNA contained two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 36-39; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-MAR-1990;
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374 YLGIKDREVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQ
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                                iigvdedgayl---apdnvitsttkdvgral----nift--snhlktntfeggk---li
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                                                              LIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATV 373
                                                                                                                              DKI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQ--NDRY 313
                                                                                                                                                            gyiaakl-----sktgkigflggiegeivdafrygyeagakyan----kdikist
                                                                                                                                                                                                                             fyrfsdvakvaalqnpdmkyai-----idpiysndpip-anlvgmtfraeegaflt 142
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Pred. No. 0.00021;
'0; Mismatches 134
                                                                                            -iihhaaglggigaievakelgsghy
                                                                                                                                                                                                                                                                                                                                                           134;
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Db 286 nyglkegvvgfv----rnpkmisf-----elekeidnlsskiinkeiivp----- 326

Qy 434 PDKQQESLDKLITD 447

:| | :| :
Db 327 --snkesyekflke 338
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Search completed: July 18, 2002, 15:32:18 Job time: 185 sec

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                       Title:
Perfect score:
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US-09-676-249A-2
2299
1 MKKKIKWNKFLGLGLVFPLS......KQPDKQQESLDKLITDINKN 451
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Copyright (c) 1993 - 2000 Comp
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Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Tmum DB BB seq length: 0 length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pir2:*
pir3:*

Database :

PIR_71:*

pir1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No. Score Match Length DB ID No. Score	ABC transporter xy lipoprotein [impor conserved hypothet basic membrane pro probable lipoprote hypothetical prote ABC transporter [impor aBC transporter [immor aBC transporter [immorane pro basic membrane pro basic membrane lipoprote basic membrane ro basic membrane ro coll-stimul	Length DB ID 461 2 B90555 350 2 G95097 374 2 C97965 350 2 F86804 357 2 D96986 516 2 C93946 516 2 C70009 350 1 F77418 517 2 F77418 341 2 F77418 341 2 F7747 357 2 AH1610 359 2 F77448 524 2 C82914 524 2 F77448 525 2 C82914
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45	43	42 42	40	39	38	37	36	3 5	34	33	32	31	30
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exported protein dnak-type molecul	lipoprotein	probable transgly	flagellar hook-as	flagellar hook-as:	protein K10D2.	probable type :	colicin Ia - Esch	ABC transporter	rhoptry protein	()	hemolysin [import	hypothetical prote	hypothetical prote

ALIGNMENTS

A;Gene: MYPU_3460 A;Genetic code: SGC3 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: B90555 ABC transporter xylose-binding lipoprotein [imported] - Mycoplasma pulmonis (strain C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 A;Cross-references: GB:AL445566; PID:914089760; PIDN:CAC13519.1; GSPDB:GN00153 A;Experimental source: strain UAB CTIP A; Molecule type: DNA A; Residues: 1-461 < KUR> A; Status: preliminary C; Accession: B90555

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QΥ 밁 δ В δÃ 밁 Ωy В δÃ 밁 δÃ 밁 Ş Query Match Best Local Similarity Matches 167 160 QLETEKNIIILGIDWTDTEN-VIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTK 218 : | | : | : | | | | : : | 334 TSILKNLGYSVFSVLSDLYT------KKSNSRNLAGFEFGKKSATVYLGIKDRFVDIA 385 107 KSQNKEAENQHKLDNYINSAVKDLEQNYKVALDRGYTTWILTGFQQGNEIENFLNDENNL 166 114 TS-------VDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENK 52 VTETQKIVENKIKQASLETQK-----VVLITADGNIDDKSFNQQVYESQKTLKDFVDKAY 106 62 1 MKLNK--KLESILEVAALAIALPATE------VSCAQNENKTNSNLDSSKITDLLSQKE 51 5 IKWNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQIT--DVSKISGLVNER- 61 ERLEQIASKDKPSTLLAVAGPLTEIFSDII---ANQNDRYLIGVDTDQSLVYTKTKNKFF 333 RAISAFGGGDFAGVTDFLNGFFEGIRAWNSEAENANKKVKIVSENLVLDTGF-IPNAEKN 285 RSAIVIGGGISPAVTDEIAGYLAGIKAWN--LKNSDKKTKITTDKIEINLGEDVQDTSTK 276 RRFKENKVKIIGVDWAPNANSKIPQGSLISLLFKTEEAGWQAGYASADFLGTKYANNEAK -----KSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEI 113 EVVSNVVETGKSTISLPVAGPFTGVVVDVLRKDTSDEDRFIVGVDTDQSLSFTNDSKRFF Conservative 24.1%; Score 554.5; DB 2; 30.3%; Pred. No. 9.6e-27; tive 88; Mismatches 175; Length 461; Indels Gaps 226 159 13;

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346

TSIVKNIAFPVYQILLALLTKDEESVILKEGNDKFLGS---NPKNLVLKRGLSAKFVNIT

Matsushima,

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McAhren,

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conserved hypothetical protein spr0747 [imported] - Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001 C;Accession: C97965
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHo
                                                                                                                RESULT
C97965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipoprotein [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: G95097
C;Accession: G95097
n, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison a;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison eference number: A95000; MUID:21357209; pMID:11463916
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A; Residues: 1-350 <KUR>
A; Cross-references: GB: AEO05672; PIDN: AAK74976.1;
A; Experimental source: strain TIGR4
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                                                                                                                                                                                                                                                                                          VSTLKQVGTTVKDI------SNKAERGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEG
                                                                                                                                                                                                                                       KKLATEAISEAKKEFEEKTKTIP
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%; Pred. No. 1.7e-06;
.63; Mismatches 148;
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J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C. A;Title: Genome of the Bacterium Streptococcus pneumoniae A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: C97965
                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-350 <STO>
A;Cross-references: GB;
                                                                                                               A;Title: The complete genome sequence of the lactic acid A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Accession: F86804
                                                                                                                                                                       R;Bolotin, A.; Wincker, P.; Mauger, S.; Genome Res. 11, 731-753, 2001
                                                                                                                                                                                                                            basic membrane protein A [imported] - Lactococcus lactis subsp. lactis (strain C;Species: Lactococcus lactis subsp. lactis C;Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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A; Gene: spr0747
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A; Residues: 1-374 < KUR>
A; Cross-references: GB: AE007317;
                  A; Experimental source:
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Best Local S
Matches 109
Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKKIKWNKFLGLGLYFPLSAIATIS-AGCWDKETTKEEKSADNQNKQITDVSKISGLVN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                VSTLKQVGTTVKDI-----SNKAEKGEFPGGQ---VIVYSLKDKGVDLAVTNLSEEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---IVYQVAGGTGAGVFAEAKSLNESRPENEKVWVIGVDRDQEAEGKYTSKDGKESNFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSSTAELE------GKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNI 167
                                                                                                                                                                                                                                                                                                                                                                                                        KKLATEAISEAKKEFEEKTKTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KPSTLLAVAGPL-TEIFSDIIANQNDR-----YLIGVDTDQSL--VYT----KTKNKFF 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I-SPAVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKD 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLIDDVIKDQKNV-----ASVTFADNESGYLAGVAAAK-----TTKTKQVGFVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FQSTSEADYANNLQQAAGSYNLI------FGVGFALHNAVEEVAKEHTDLNY 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IESEVISRFEAGFKAGV-----ASVDPSIKVQVDYAG-SFG-DAAKGKTIAAAQYAAGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGA---LTGGEITSV 116
                                                                                                                                                                                                                                                                                                                                                                         -AVEDAKAKILDGSVKVP
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                  GB:AE005176; PID:g12724428; PIDN:AAK05536.1; GSPDB:GN00146
ce: strain IL1403
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; Pred. No. 3.3e-06;
62; Mismatches 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:AAK99551.1;
                                                                                                                                                                                                                                                                                                                                                                                                            416
                                                                                                                                                                                         Jaillon,
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                                                                                                                                                                                         Malarme, K.;
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Strain R6
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                                                                                                                                                                                         Weissenbach,
                                                                                                                                                     Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.H.;
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Match

9.08;

Score

207;

DB

2

Length

350;

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probable lipoprotein, Med/BMP family [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C; Accession: D96986 R; Nolling, J; Breton, G; Omelchenko, M,V.; Markarova, X.S.; Zeng, Q.; Glbson, R; Nolling, J.; Benett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001 A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacte A; Accession: D96986 A; Accession: D96986 A; Accession: D96986 A; Status: preliminary A. Molecula trace. Nas
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Best Local Similarity
Matches 100; Conser
                                                                                                                                                                                                                                                                                                          Molecule type: DNA lesidues: 1-357 <KUR> lesidues: 1-357 <KUR> cross-references: GB.AE001437; PIDN:AAK78679.1; PID:g15023581; Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 107; Conserv
                                                                                                                                                                                                                                                                                   Genetics:
Gene: CAC0702
                                             121
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                                                                                                                                                                      1 MKKKIKWNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNE
                                             A-ELEGKYSSLANTNKNVWVLSGFQHGDAF-TRWLKIPENKQLFTE-----KNIIILG 171
                                                                                              RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LATEAISEAKKEFEEKTKTIPAE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLAVAGPL-TEIFSDIIA-----NQNDR-YLIGVDTDQSLV--YT----KTKNKFFTSIL
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                                                                                                                                        IKKKT-----STSSGSGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---DAVAKAKADIIDGKITVPSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVTDFTAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVIKDQKNV-----ASATFADNESAYLAGVAAAK-----ATKTNKIGFIGGMQSD 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EITSVDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILG
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                KDDYQPNLQSLIDNDSDLVFGVGYQMADDLATIAKKYPDKKFAIIDDAYDKQPKNI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEVG----NVVKDIADKTKDGKFPGGTIVTYDLKNGGVNLGL-----DSANSEIK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYQCAGGVGTGVFSEAKALNSTKNEADKVWVIGVDQDQEYLGKYKSKDGKDSNFVLVSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDWIDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPIKRSAI-VIGGGISP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107;
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                                                                                                                                                                                                      Conservative
                                                                          DTKK---VKVGLSTDEGGLNDKSFNQGADEGIKKAAKEYSVDYKAIESKK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKTD-----LKAAIVTEIGGVNDRSFNQSAWEGL()SWGKENNLKKGTG
                                                                                                                                                                                                                   8.5%; Score 195.5; DB 2; 22.3%; Pred. No. 8.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.28;
                                                                                                                                                                                                   72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.7e-05;
2; Mismatches 156;
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                      156;
                                                                                                                                                                                                     Indels 121;
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A;Gene: UU012
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A;Molecule type: DNA
A;Residues: 1-516 <GLA>
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Best Local (
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A;Cross-references: GB:AE002100; GB:AF222894; NID:g6898946; PIDN:AAF30417.1; GSPDB:GN A;Experimental source: serovar 3; biovar 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, February 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein UU012 [imported] - Ureaplasma urealyticum C;Species: Ureaplasma urealyticum C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_changeC;Accession: C82946
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                                                  324 VYTKTKNKFFTSIL---KNLGYSVFSVLS--DLYTKKSNSRNLAGFEFGKKSATVYLGI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 KYKKAIIDGKIVVPDTVDKAQTFKTDQIK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AE-LEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQ--LFTEK---NIIIL---G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKKIKWNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNE
                                                                                                                                                                                                                                                                                                                             VYNNDNKAEFYKGADRVADVYFKVDEAAFLGGIAAAYMLNSNQAVFGAD----NKLTWGG
                                                                                                                                                                                                                                                              --GISPA-VTDFIAGYLAGIKAWNLKNSDKKTK---ITTDKIEINL-----
                                                                                                                                                                                                                                                                                                                                                            IDWTDTENVIPTG---RYINLTYKTEEAGWLAGYANASFLAKK---FPSDPTKRSAIVIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKKLNKKVLFLAIGSVFALGTIITVATSCTQKSTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K------EFEEKTKTIPAEEVR 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VYHAAGGAGIGVF-DVAKSLRDQGKDVWAIGVDKDQAAGLPKYADVILTSMVKRVDIATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLLAVAGPLTEIFSDIIANQNDR----YLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDSANAKKIIQELITKG-ADLILPVAIPQVGIAVTEAIATTSHNVGVIGVDVEIENDQAI
                                                                                                                                                                                                                 YVGINAKNTTNYLAGFDLGVKWANEKLKDKNIKQEGTQETKKWINVEQVYASESSAGGFQ 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSST 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LINKFLSGYIAGAKTVN-----PNITVEK---NYTNDYSDTSKGKEVATSLYNGGCDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISP
-- NKKTDKFINTHLSGNKN-GVIRFSITKRLDTATIKLLENAIKGESLSKKSDQIVIGSE
                                                                                                                                                        VQDTSTKERLEQIASKDKPSTLLAVAGPLTEI-FSDIIANQNDRY-LIGVD----TDQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                     DEGFQTKYKSMASDGKRALLMPGYQH------PERLQNALVNDKFDPNLIALILDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----FEGGKVES---FGLKEDGVGVAPTS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -MSLVFKEQEGSFLMG-----VIAGKM----TKTNKIGFVGGKDQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 187.5; DB 2;
Pred. No. 0.00046;
7; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---NYSQFYW---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TSPTSDD
                                                                                                                                                                                                                                                                    -GFD
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                                                                                                        274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
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C:Accession: C70009

R:Kunst, F: Ogasawars, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Che Ebrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. ure 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mullo, M.F. Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schrocter, R.; Scoffone, F.; Sekiguchi, J.; Sckowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toganoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Aithors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Seror A; Reference number: A6580; MUID:98044033

A:Startus: pre-liminary. purcleic acid sequence of the Gram-positive bacterium Bacillus subtilis. A; A; Carter acid sequence of the Gram-positive bacterium Bacillus subtilis.
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C; Superfamily: ABC transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABC transporter (lipoprotein) homolog yufN - Bacillus subtilis C;Species: Bacillus subtilis C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           est Local Similarity
atches 106; Conserv
                                                                                                                                                                     187
                                                                                                                                                                                                                                                                  139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 AIATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKSEIMAAKADANKHFGLNM 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
AIVTAGGTVNDNSFNQSSWEAIQQLGALTG-----GEITSVDSSTAELEGKYSSLANTN 134
                                                                         KKEDPKRDVWVIGVDKDQYAEGQVEGTDDNVTLTSMVK----KVDTVVEDV-TKKASDGK 291
                                                                                                                                                                                                                                                                                                                                                                                                        KNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGID-WTDTENVIPTGRYINLTYKT 193
                                                                                                                                                                     ----AVVEVKYAGGFDKADVGKATAESM----YKSGVDVIYHSAGATGTGVFTE-AKNL
                                                                                                                                                                                                               KKTKITTDKIEINLGFDVQDT--STKERLEQIASKDKPSTLLAVAGPL-TEIFSDIIAN-
                                                                                                                                                                                                                                                                QEGSFLVGVAAAL-----SSKSGKIGFVGGMESELIKKFEVGFRAGVQAVNPK---
                                                                                                                                                                                                                                                                                                              EEAGWLAGYANASFLAKKFPSDPTKRSAI-VIGGGISPAVTDFIAGYLAGIKAWNLKNSD
                                                                                                                                                                                                                                                                                                                                                          FDLIYGVGYLMEDSIS---EIADQR-----KNTNFAIIDAVVDKDNV-----ASITFKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGTILGACGNSE--KSSGSGEGKNK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVRKTLEIPEMPDKQPDKQQES 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMVTDVGGVDDKSFNQSAWEGIQAFGKENGLKKGKNGYDYLQSKSDADYTTNLNKLAREN
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                                                                                                                     -QNDRYLIGVDTDQ----SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.1%;
24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; GB:AL009126; 1
1 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 185.5; DB 1;
Pred. No. 0.00035;
1; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
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A; Accession: A43595
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A; Residues: 1-353 <COL>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 MAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSST-AELEGKYSSLANTNKNVW 138
                                                                                                                                                                                                                                            TKITTDKIEINLGFDVQDT-STKERLEQIASK---DKPSTLLAVAG----PLTEIFSDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGMVTDSGDIDDKSFNQQVWEGISRFAQENNAKCKYVTASTDAEYVPSLSAFADENMGLV 101
                                                                                                                                                              ANQNDRYLIGVDTDQSL--VYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGF
                                                                                                                                                                                                                                                                                                           LVGVA-AALKAKE-----AGKSAVGFIVGMELGMMPL---FEAGFEAGVKAVD-----
                                                                                                                                                                                                                                                                                                                                                                                                      VACGSFLVEA-----VIETSARFPKQKFLVIDAVVQDRDNV-----VSAVFGQNEGSF
                                                                      EFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTL 424
                                                                                                                                                                                                                                                                                                                                                     LAGYANASFLAKKFPSDPTKRSAI--VIGG--GISPAVTDFIAGYLAGIKAWNLKNSDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGW 198
                                                                                                                       LNGQDVWVIGVDRDQYMDGVYDGSKSVVLTSMVKRA-----DVAAERISKMAYDGSFPG-
                                                                                                                                                                                                                 -----PDIQVVVEVANTFSDPQKGQALAAKLYDSGVNVIFQVAGGTGNGVIKEARDRR
                          -GQSIMFGLEDKAVGIPE----ENPNLSSAVMEKIRSFEEKI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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```

69; Mismatches 134;

Indels

74;

Gaps

17;

364

300

254 149

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membrane lipoprotein TmpC precursor - syphilis spirochete (;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete) C;Date: 07-Aug-1998 #sequence_revision 07-Aug-1998 #text_change 23-Jul-1999 C;Accession: H71340; A43595; S29561
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dods rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterbethey, L.; Weidman, J.; Smith, H.O.; Venter, J.C. Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spiroc A;Reference number: A71250; MUID:98332770
A;Accession: H71340
                                                                                                                                C;Keywords: blocked amino end; lipoprotein; membrane protein; thiolester F;1-20/Domain: signal sequence #status predicted <SIG> F;21-353/product; membrane lipoprotein tmpC #status predicted <MAT> F;21/Modified site: fatty acylated amino end (Cys) (in mature form) #status F;21/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status predict
                                                                                                                                                                                                                                                                                                            A;Gene: tmpC; TP0319
A;Start codon: GTG
C;Superfamlly: ABC transporter yufN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-10, 'A', 12-158, 'R', 160-353 <SCH>
A; Cross-references: GB: X57836; NID: 948838; PINN: CAA40968.1;
A; Note: this protein is shown to incorporate palmitic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Infect. Immun. 59, 3536-3546, 1991
Infect. Immun. 59, 3536-3546, 1991
A;Title: Characterization of the 35-kilodalton
A;Reference number: A43595; MUID:91372962
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7.9%;
23.7%;
Score 182; DB 1;
Pred. No. 0.00058;
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                                           basic membrane lipoprotein B (bmpB) - Lyme disease spirochete C. Species: Borrelia burgdorferi (Lyme disease spirochete) C. Species: Borrelia burgdorferi (Lyme disease spirochete) C. Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999 C. Accession: E70147; I40290; I40242 R. Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hature 390, 580-586, 1997
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  Nature 390, 580-58
A; Authors: Smith,
A; Title: Genomic s
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Best Local S
Matches 94
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Residues: 1-359 <ARN>
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Sene: TM0102
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     spirochaete,
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A; Authors: Krook, C.; Schlu
                                                                                           C;Species: Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 2
C;Accession: AH1610
R;Glaser, P.; Frangeul, L.; Buchrieser,
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                                                                         Dominguez-Bernal,
; Jones, L.M.; Kars
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Schlueter,

Kuhn, M.;
; Simoes, N 2001

, Kunst, F.; N.; Tierrez,

Kurapkat, G.; Madueno, , A.; Vazquez-Boland, J

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Maitournam, A.;
Voss, H.; Wehla

)4, 849-852, : : Kreft, J.; !

Karst,

Durand,

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Baquero, F surget, O.;

F.; Berch; Entian,

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27-Nov-2001 C.; Amend,

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R;Ojaimi, C.; Davidson, B.E.; Saint Girons, Microbiology 140, 2931-2940, 1994
A;Title: Conservation of gene arrangement ar A;Reference number: I40241; MUID:95111614
A;Accession: I40242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-44,'A',46-179 <RE2>
A;Cross-references: GB:L35050; NID:g516591;
C;Superfamily: basic membrane protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-232, 'A', 234-317, 'V', 319-341 < E
A; Cross-references: GB:L24194; NID:9508420;
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A;Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: AE001143; A; Experimental source: strain B31
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Residues: 1-34
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Accession: E70147
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KVLERKIINKEIIVP
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                                                                     IKNNNV-----WEGGK----VVQMGLRDGVIGLPNAN-
                                                                                                                                                AAGLAGIGVIETAKNLGDGYYVIGADQDQS--YLAPKN-FITSVIKNIGDALYLITGE-Y
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                                                                                                                                                                                                                                                          AGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASK--DKPSTLLAV
                                                                                                                                                                                                                                                                                                A-----VVFRVEQGAFLAGYIAAKKSFSGK-----
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I.; Old, I.G.
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A; Molecule type: DNA
A; Residues: 1-360 <KLE>
A; Cross-references: GB: AE001144; GB: AE000783;
A; Experimental source: strain B31
C; Superfamily: basic membrane protein C
                                                                                                                                                                                                                                                              C. membrane protein D (bmpD) homolog - Lyme disease spirochete
C. Species: Borrella burgdorfer! (Lyme disease spirochete)
C. Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 29-Sep-1999
C. Accession: H70147
R. Fraser, C.M.; Clasjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Soon, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujli, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A;Accession: A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GLA>
A;Cross-references: GB;AL592022; pIDN:CAC96656.1;
A;Cross-references: GB;AL592022; DIDN:CAC96656.1;
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                                                                                                                                                                                                          Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease
A;Reference number: A70100; MUID:98065943
A;Accession: H70147
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                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence
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VYLGIKDREVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMP
                                                                                                                                                                                                                                                                                                                                                                                                                                               IEYGLDKDAVGLSE-----HQDNISKDVLAKVE---EYKQKIVDGD-----IKVPEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DQ-----SLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSAT
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|| : : || : || | || :||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGLV-----NERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQWDEGKVTANDGKDYNVTLTSEIKRVDIAV----DDLAT----RTKAGDFPGGTK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALT----GGEITSVDSSTAELEGKYSSLANTNKNVWVLS------GFQHGDAFTRWLK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - IPENKOLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFP
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                                               Conservative
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                                                          7.48;
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                                            Score 169.5; DB
Pred. No. 0.0035;
4; Mismatches 13
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                                                                                                                                                                                                                                       spirochaete,
                                                                                                                                                                                             not shown;
                                                                                                                                                 NID:g2688291; PIDN:AAB91505.1; PID:g26882
                                                                         DB 2;
                                            137;
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; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; E.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AD1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD1248
C;Accession: AD1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Glaser, P.; Frangeul, L.;
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                                                                                                                                                                                                                                                              AIVDDTI------DDRDNVVSIG-----FKDNDGSYLVGVVAGL-----TTKTN
                                                                                                                                                                                                                                                                                                         LFTEKNIIILGIDWIDTENVIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRS
                                                                        DKGQQIASSMYSSGVDVIFHAAGGTGNGVFAE-AKNLKKKDPSRAVWVIGVDRDQWDEGK
                                                                                                                                                                    KVGFVGGVKGTVIDRFEAGFTAGVKA
                                                                                                                                                                                            AIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQ---DTSTK 276
                                                                                                                                                                                                                                                                                                                                                        GTDGYNYLQSASEADYK-----TNLNTAVRSDYDLIYGIGYKLKDAIEEVSKQKPKNQF
                                                                                                                                                                                                                                                                                                                                                                                                   GGEITSVDSSTAELEGKYSSLANTNKNVWVLS-----GFQHGDAFTRWLK-IPENKQ 160
-SLYYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAG-FEFGKKSATVYLGIKD
                                                                                                                 ERLEQIASKDKPS----TLLAVAGPLTEIFSDIIANQNDR-----YLIGVDTDQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGIGVIEAAKELGPDHYIIGVDQDQSYL---APNNVIVSAVKKVDSLMYSL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 169; DB 2;
Pred. No. 0.0037;
3; Mismatches 14
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                                                                                                                                                                  -VNPNAQIDVQYANDFAKA
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Lian, K.D.; 1
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Voss, H.; Wehla
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell,
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  hypothetical membrane C; Species: Ureaplasma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
Residues: 1-525 <GLA>
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Best Local (
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Xperimental source: serovar 3; biovar 1
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                                                                                                                 411 KSQQGDWVLKS-EYQDLPFIQLQKMLGGLVYVDQKNELYPYELSNSIYLEKDPNKRQAS 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UU226
                                                                                                                                                                                                                                                                                                                                                                                        QIASKDKPSTLLAVAGPLTEIFSDIIANQNDR-YLIGVDTDQSLVYYKTKNKFF--TSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKIKLNKKIILASVIGIMGVALVPIAL------VACSQNKTK;SDSRNLT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TG--RYINLTYKTEEAGWLAGYANASFLAKK---FPSDPTKRSAIV:GGGIS---PAVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -------LNNFYG-------RPSSDGDDAYQAI-----
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                                                                                                                                                                                                                                                                         ANGKTIIFSIVKRLDLAFKGALLKASEGAQLINDINKDAYKLGTHT!:ASF--NKNTYVD-
                                                                                                                                                                                                                                                                                                             KNLGYSVFSVLS--DLYTK-----KSNSRNLAGFEFGKKSATVYLGIKDRFVDI
                                                                                                                                                                                                                                                                                                                                                    QLVS-NNVDLILPVAGPQIDYATTAAAESSKPIVVVGVDTEQELDDHTNKARISENNKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                 FIQGFKFGIQWANEKLKNKKVKQTENNEEKEWINVEQVFATNYQSGIJFSPTSDKAKAIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----YASKIQDGARMLGLISFRHKNPISKYFNSPKDNQ---QVSAVLI-----DEIYDLQ 119
                                                                                                                                                         KTIPAEEVRKTLEIPEMP--
                                                                                                                                                                                                                                    ADTSL----
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                                                                                                                                                                                            -NTALVELSKAGHQYLIDAIKLSGLKEVNDYKTIVEIIQEDPLFKL1.SQIGTKKLDEVAT
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lipoprotein UU016 [imported] - Ureaplasma urealyticum urealyticum \ensuremath{\mathsf{U}}
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                                                                                                                                                                                                                                    -EGNDKKLATEAISE-----
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                                                                                                                                                         -DKQPDKQQES 440
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A;ResIdues: 1-524 <GLA>
A;Cross-references: GB:AE002101; GB:AF222894; NID:96898957; PIDN:AAF30421.1; GSPDB:GN
A;Experimental source: serovar 3; biovar 1
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C;Accession: D82944
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.;
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                                   KTKTIPAEEVRKTLEIPEMPDKQPDKQQESLDKLI 445
                                                                                                                                                                                                                                                                                                                                     DFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKER----LEQI-ASK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKSKINKKILFASLAGVVTLTSVAAIAASCND----SNKDDGKTNKDGNYISKLS----
KGTTKLEDLATKTSDGWVLKDSEKNKSFSELQKLL
                                                                         SL----DKSTYVDDTPLVELSNAGRVYLEQAAKLAGLKAITYAQIVNVIQNEELFKLLST
                                                                                                                                                  VTNRKRITNKTVNDGKTILFSIVKRVDLAMKGAIENASKGAQLTNDINKDAYKLGTHTEA
                                                                                                                                                                                      ----VYTKTKNKFFT---SILKNLGYSVFSVLSDLY--TKKSNSRNLAGFEFGKKSAT
                                                                                                                                                                                                                           GSFKPDEEGATNIINDLITKKADVILPVAGPQTNLATSIVSNATDPSVIIGVDTAQELDD
                                                                                                                                                                                                                                                             TFIQGFKLGVQWANEKLKDK-----EIN----QEDANGSKKKWMNVEQVFASKYVA
                                                                                                                                                                                                                                                                                                                                                                             -VGKDRIASVSYRVDQAAFLTGIAAAYYLNANQKTFAAD----GKLTWGGYVGLHFTSTS
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                                                                                                             VYLGIKDREVDIADTS-----KEFEE 410
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21.0%;
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Pred. No. 0.013;
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                                                                                                                                                                                                                       LIPID
SEQUENCE
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15-DEC-1998
16-OCT-2001
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EMBL; Z99120; CAB15143.1; -.
Subtilist; BG12349; yufN.
InterPro; IPR003760; Bmp.
Pfam; PF02608; Bmp; 1.
PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
Bacteria; Firmicutes; Ba
Bactlus/Staphylococcus
NCBI_TaxID=1423;
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Submitted (APR-1997) to
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                                                                                                                                                                                                                                                                          SIGNAL
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                                                                                                                                                                                                                                                                                                            Hypothetical protein; Membrane;
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(Potential).
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l lipoprotein yufN precursor.
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                                                                                                                                                                                                                         WW;
                                                                                                                                     61;
                                                                                                                                 Score 185.5;
Pred. No. 0.00
61; Mismatches
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WAPA_STRMU
PARC_BORBU
YD86_SCHPO
SLA2_BACAN
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XCPC_XENLA
MSP1_PLAFF
MSP1_PLAFM
CEIB_ECOLI
YG51_YEAST
M6_STRPY
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HYPOTHETICAL LIPOPROTEIN YUFN.
N-ACYL DIGLYCERIDE (PROBABLE).
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plasmodium
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Result No.

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Query Match

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7 borrelia su
4 treponema p
1 borrelia bu
7 listeria in
2 borrelia su
3 borrelia bu
4 listeria mo
5 borrelia af
5 borrelia bu
6 mycoplasma
6 borrelia bu
9 streptococc

Description

SUMMARIES

YUFN BACSU
BMPA_BORGA
TMPC_TREPA
TMPB_BORBU
TCSA_LISIN
BMPB_BORBU
TCSA_LISMO
BMPA_BORBU
TCSA_LISMO
BMPA_BORBU
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TCSA_LISMO
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TCSA_LISMO
BMPC_BORBU
TO40_MYCGE
BMPB_BORBU
TO40_MYCPN
CEIA_ECCUI
TCGK_SALTY
LBPA_NEIMB
YKDA_MYCCA
PKSL_BACSU
TCGCU
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TCGK_STRAG
ANT1_ONCVO
BAG_STRAG
ANT1_VEAST
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RPOB_ASTLO
LBPA_NEIMB
YA47_SCHPN

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15-DEC-1998 (Rel. 37, C
15-DEC-1998 (Rel. 37, L
15-DEC-1998 (Rel. 37, L
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                 Pfam; PF02608; Bmp; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roessler D., Hauser U., Wilske B.; "Heterogeneity of BmpA (P39) among European burgdorferi sensu lato and influence of inte
                                                                                                                                                                                                                   InterPro; IPR003760; Bmp.
InterPro; IPR000437; Prok_lipoprot.
                                                                                                                                                                                                                                                                  EMBL; X97244; CAA65883.1; -. EMBL; X97238; CAA65877.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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NCBI_TaxID=29519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borrelia garinii.
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FUNCTION: NOT KNOWN; IMMUNOGENIC PR
SUBCELLULAR LOCATION: Attached to t)
(Probable).
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PROBABLE.
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S -> N (IN STRAIN PLI).
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                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-NICHOLS; MEDLINE-98332770; F
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                  Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J. Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garlan Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.
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STRAIN-NICHOLS;
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Bacteria; Spirochaetales;
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  г J.
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Pred. No. 0.00012;
6; Mismatches 135
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Q45011; 007954; 031317; 050168; Q44858;
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15-DEC-1998 (Rel. 37, Last sequence upd
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Science 281:375-388(1998).
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SIMILARITY: BELONGS
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S29561; S29561.
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Pr02608; Bmp; 1.
Pr02608; Bmp; 1.
ProckaR_LIPOPROTEIN;
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MEDLINE-98065943; PubMed-9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.P.

Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K.,

Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

Peterson J., Kerlavage A.R., Quackenbush J., Saizberg S., Har

van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Meidman J.,

Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,

Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatc
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STRAIN-ATCC 35210 / B31;

MEDLINE-98010210; PubMed-9350727;

Roessler D., Hauser U., Wilske B.;

"Heterogeneity of EmpA (P39) among European isolates burgdorferi sensu lato and influence of interspecies serodiagnosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94327086; PubMed-8050720; Simpson W.J., Cieplak W., Schrumpf M.E., "Nucleotide sequence and analysis of the encoding the immunogenic P39 antigen."; FEMS Microbiol. Lett. 119:381-388(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Conservation of gene arrangement and an unusual organization of genes in the linear chromosomes of the Lyme disease spirochaetes Borrelia burgdorferi, B. garinii and B. afzelli.";
Microbiology 140:2931-2940(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Garland S., Fujii C., Smith H.O., Venter J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=ATCC 35210
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Aron L., Toth C., Godfrey H.P., Cabello F.C.;
"Identification and mapping of a chromosomal oburgdorferi containing genes expressed in vive FEMS Microbiol. Lett. 145:309-314(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=212;
MEDLINE=95111614; PubMed=7812434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, I
Basic membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genomic sequence of a Lyme burgdorferi.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Probable).
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION:
; L24194; AAA72407.1; -.
; U4993B; AAC44713.1; -.
; X81517; CAA57237.1; -.
; AE001143; ACC66758.1; -
; L35050; AAC41402.1; -.
; BB0382; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           390:580-586(1997).
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                                                                                                                                                                                                                        nd this statement is not remo equires a license agreement ( email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-179
                                                                                                                                                                                                                                                                                                                                                                                     entry is copyright.
iss Institute of Bio
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Spirochaetaceae; Borr
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Best Local Similarity
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SEQUENCE FROM N.A.

STRAIN-CLIP 11262 / Serovar 6a;

STRAIN-CLIP 11262 / Serovar 6a;

MEDLINE-21537279; PubMed-11679669;

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget Centian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson I Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
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CONFLICT
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PROSITE; F
Membrane;
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01-MAR-2002 (Rel. 41,
01-MAR-2002 (Rel. 41,
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Bacteria; Firmicutes;
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TE; PS00013;
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13; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD
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Last annotation updat
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Pred. No. 0.000
59; Mismatches
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-> A (IN STRAIN 212).

-> T (IN STRAIN B31).

-> I (IN STRAIN B31).

-> P (IN REF. 3).

-> P (IN REF. 3).
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Best Local
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                                                                        15-DEC-1998
15-DEC-1998
15-DEC-1998
       Borrelia garinii.
Bacteria; Spirochaetales;
NCBI_TaxID=29519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIPID
SEQUENCE
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SIGNAL
CHAIN
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the Euro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL596168; CAC96656.1; L1stiList; LIN01425; -.
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ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
by non-profit institutions as long as i
ified and this statement is not removed. Us
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                                                                                                                                                                                                                VYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMP
                                                                                                                                                                                                                                                                                                                                           --TTKTNKVGFVGGVKGAVIDRFEAGFTAGVKA---
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                                                                                                                                                                                        IEYGLDKDAVGLSE-----HQDNISKDVLAKVE---EYKQKIVDGD-----IKVPEKP
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                                                              membrane
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E; PS00013; PROKAR_LIPOPROTEIN; 1.

n; Membrane; Lipoprotein; Signal; CC
pROBABLE
2 PROBABLE
3 357 CD4+ T CELL-
N-ACYL DIGLY
N-ACYL DIGLY
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357
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                                                            protein
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Last annotation update)
n B precursor.
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                       Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
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Pred. No. 0.000
62; Mismatches
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N-ACYL DIGLYCERIDE (PROE
; 2EDA2AA9820A3FBC CRC64
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.00058;
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Best Local 9
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Q44743;
15-DEC-1998 (
15-DEC-1998 (
16-OCT-2001 (
Borrelia burgdorferi (Lyme Bacteria; Spirochaetales; S NCBI_TaxID=139; [1]
                                                 Basic membrane protein BMPD OR BB0385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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-!- SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serodiagnosis.";
J. Clin. Microbiol. 35:2752-2758(1997).
Attached to the membrane
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(Rel. 40,
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ty of BmpA (P39) among European isolates
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                          Spirochaetaceae; Borrelia
                                      disease
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N-ACYL DIGLYCERIDE (PRO
; 442BEF0BFEDDOC9A CRC6
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Pred. No. 0.
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variability
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Best Local
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STRAIN-ARCC 35210 / B31;

MEDLINE-98065943; PubMed-9403685;

MEDLINE-98065943; PubMed-9403685;

Iathigra R., White O., Retchum K.A., Dodson R., Hickey E.K.

Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,

Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S.,

Peterson J., Kerlavage A.R., Googne J.D., Weidman

Utterback T., Walthey L., McDonald L., Artiach P., Bowman

Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., H

Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                      LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ramamoorthy R., Povinelli L., Philipp M.T.; Molecular characterization, genomic arrangement, and bmpD, a new member of the bmp class of genes encoding proteins of Borrelia burgdorferi."; Infect. Immun. 64:1259-1264(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic sequence of a Lyme disease spirochaete, burgdorferi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02608; Bmp; 1.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Attached to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 390:580-586(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - I - SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS
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   357
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                                                                                                                                                                                                                                                                                                 65 IMAAKADANKHEGINMAIVTAGGTVNDNSFNQSSWEAIQQIGAITGGEITSVDSSTAELE 124
                                                                                                                                                                                                                                                                                                                                                              Match
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                                                                                                                                                                 GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTD-FIAGYLAG
                                                                                                                                                                                                                                                                     VACSSSDDGKSEAKTVSLI-VDGAFDDKGFNESSSKAIRKLKADLNINIIEKASTGNSYL
 NSRNLAGFEFGKKSATVYLGIK-DRFVDIADTSLEGNDKKLATEAI
                                              TEIFSDIIANQ--NDRYLIGYDTDQSLYYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKS
                                                                                                                    IKAWNLKNSDKKTKITTDKI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPL
                                                                                                                                                                                                          GDIANLEDGNSNLIWGI-GFRLSDIL--FQRASENVSV----NYAI--IEGVYDEIQIPK
                                                                                                                                                                                                                                       GKYSSLANTNKN-VWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPT
                               SGIGVIEAAKELGPDHYIIGVDQDQSYL---APNNVIVSAVKKVDSLMYSL-
                                                                                                                                                  - NLLNISFRSEEVAFLAGY - - - - - - FASKASKTGKIGFVGGVRGKVLESFMYGYEAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003760; Bmp.
                                                                                                                                                                                                                                                                                                                                                                                                        341 AA;
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17
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                                                                                                                                                                                                                                                                                                                                             7.48;
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                                                                                                                                                                                                                                                                                                                                           Score 169.5; DE Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                      BASIC MEMBRANE PROTEIN D.
N-ACYL DIGLYCERIDE (PROBABLE)
; 63FF6638F81A91D5 CRC64;
                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                               137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collaboration
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                                                                                     Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                Antigen;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
Science 294:849-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL591979; CAC99466.1; -. EMBL; S80336; AAB35725.2; ALT_TERM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *Sanderson S., Campbell D.J., Shastri N.;
"Identification of a CD4+ T cell-stimulating antigen bacteria by expression cloning.";
J. Exp. Med. 182:1751-1757(1995).
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STRAIN-EGD-e / Serovar 1/2a;
MEDLINE-21537279; PubMed-11679669;
                                                                                                                                                                                                                                           SEQUENCE
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NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                      LIPID
                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ListiList; LMO01388; -.
InterPro; IPR003760; Bmp.
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15-DEC-1998
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                           54 ISGLVNERKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALT----
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SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS.
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PF02608; Bmp; 1.

TE; PS00013; PROKAR_LIPOPROTEIN; 1.

Yen; Membrane; Lipoprotein; Signal; Complete proteome.

PROBABLE.

PROBABLE.

PROBABLE.

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                                                                                     1 Similarity 23.8%; 98; Conservative /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell-stimulating antigen precursor.
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                                                                                           63;
                                                                                     Score 169; DB
Pred. No. 0.001
53; Mismatches
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                                                                                                                                                                                                                                          EMBL; X81516; CAA57236.1; -. EMBL; X97237; CAA65876.1; -. EMBL; X97239; CAA65878.1; -. EMBL; X97241; CAA65880.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Heterogeneity of BmpA (P39) among European isolates burgdorferi sensu lato and influence of interspecies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-PKO, PWUDI, PLE, AND PLJ7;
MEDLINE-98010210; PubMed-9350727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia afzelii.
Bacteria; Spiroch
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J. Clin. Microb
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                                                                                                                         Antigen;
                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roessler D., Hauser U., Wilske B., "Heterogeneity of BmpA (P39) among
                                                                                                                                                                                                              InterPro; IPR003760; Bmp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clin. Microbiol. 35:2752-2758(1997).
FUNCTION: NOT KNOWN; IMMUNOGENIC PROTEIN.
SUBCELLULAR LOCATION: Attached to the mer
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2; PS00013; PROKAR_LIPOPROTEIN; 1.

1; Membrane; Lipoprotein; Signal.

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18 39 BASIC MEMBRA
18 18 N-ACYL DIGLY
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                                                                                                              MEDLINE=97132632; PubMed=8978084;
Aron L., Toth C., Godfrey H.P., Cabello F.C.;
"Identification and mapping of a chromosomal ge
burgdorferi containing genes expressed in vivo.
FEMS Microbiol. Lett. 145:309-314(1996).
                                                                                                                                                                                                                                                                             FEMS
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
Fraser C.M., Casjens S., Huang W.M.,
                                                                                                                                                                                                                                                                                              Simpson W.J., Cieplak W., Schrumpf M.E., "Nucleotide sequence and analysis of the encoding the immunogenic P39 antigen."; FEMS Microbiol. Lett. 119:381-388(1994).
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
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-i- FUNCTION: NOT KNOWN; IMMUNOGENIC PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K. Dougherty B., Tomb J.-F., Pleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., van Yugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman Utterback T., Watthey L., McDonald L., Artiach P., Bowman Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., H. Smith H.O., Venter J.C., "Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
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EMBL;
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LGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQP
                                                      IGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVY
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BB0383; -.
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Pred. No. 0.
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N-ACYL DIGLYCERIDE (PROBABLE).
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A9581868CA7DB923 CRC64;
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STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; PubMed-8253680;
Peterson S.M., Hu P.-C., Bott K.F., Hutchison
Peterson S.M., Hu P.-C., Bott K.F., Hutchison
Peterson S.M., Hu P.-C., Bott K.F., Hutchison
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MEDLINE-96026346; PubMed-7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Myuyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchson C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403(1995).
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EMBL; U02125; AAD12400.1;
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Bacteriol. 175:7918-7930(1993).
- SUBCELLULAR LOCATION: Attached
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                                                                    84;
                                                                  Score 156.5;
Pred. No. 0.01
34; Mismatches
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N-ACYL DIGLYCERIDE (POTENTIAL);
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                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                         or send an email to license@isb-sib.ch).
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Roessler D., Hauser U., Wilske B.;
"Heterogeneity of EmpA (1939) among European
burgdorferi sensu lato and influence of inte
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15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
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NCBI_TaxID=29518;
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SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS
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                                    Lipoprotein; Signal
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                                                             PROKAR_LIPOPROTEIN;
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BMPC_BORBU STANDARD,
050169; Q44859;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
          Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman Utterback T., Watthey L., McDonald L., Artiach P., Howman Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                         "Cloning and DNA sequence analysis of bmpC, a gene encodi potential membrane lipoprotein of Borrelia burgdorferi."; FEMS Microbiol. Lett. 123:75-82(1994).
                                                                                                                                                                                                                                                                                                                                 Aron L., Alekshun Cabello F.;
                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
                                                                                                                                                                               Aron L., Toth C., Godfrey H.P., Cabello F.C.; "Identification and mapping of a chromosomal geburgdorferi containing genes expressed in vivo. FEMS Microbiol. Lett. 145:309-314(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi (Lyme
Bacteria; Spirochaetales; S
                                                                                                                                                                                                                                    MEDLINE=97132632; PubMed=8978084;
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Nature 390:580-586(1997).
. sumcELLULAR LOCATION: Attached
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                                                               Streptococcus pyogenes. Bacteria; Firmicutes; E
                                                                                                                                           Q99XS1;
16-OCT-2001
STRAIN=SF3.70 / ATCC 700294 / Serotype
             SEQUENCE FROM N.A.
                                     NCBI_TaxID=1314;
                                                   Streptococcus
                                                                                         PEPDB OR SPY2066.
                                                                                                     Probable dipeptidase B
                                                                                                                 16-0CT-2001
16-0CT-2001
                                                                                                                                                                      PEDB_STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Membrane;
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PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PTODADLE).
-!- SIMILARITY: BELONGS TO THE BMP FAMILY OF LIPOPROTEINS
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                                                                                                                                                                                                                                                              354
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                                                                                                                                                                                                                                   289 ---NNRVFKG-----GITIDRGLKEGVIEIVKDPDVLNN--RLVDEVIDLENK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 VTAGGTVNDNSFNQSSWEAIQQLG-----
                                                                                                                                                                                                                                                           KKSNSRNLAGFEFGKKSATVYLGIKDRFVDIA-DTSLEGNDKKLATEAISEAKK
                                                                                                                                                                                                                                                                                                                                                                                         NS-LAIKFRNEEAAFLAGYIAAKMSRKE-----KIGFLTGPMSEHVKDFKFGFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGI----DWTDTENVIPT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLAHGSFYDKGYNQSVHDGVVKLRDNFGIKLITKSLRPYPIEGKRLLTVDE--AMTEDAY
                                                                                                                                                                                                                                                                                                                                        AGIFYANPKLRLVSKKAPSLFD
                                                                                                                                                                                                                                                                                                                                                                 AGIKAWN--LKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIA----SKDKPSTLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                              EVQKNPLNLFWLI-GYRFSDL-----SVKLSYERPDIYYGIIDAFDYGDIQ--VPK
                                                                                                                                                                                                                                                                                     AGITGLGVYDAAKELGPKYYVIGLNQDQSYI---APQNVITSIIKDIGKVIYSISSEYI-
                                                                                                                                                                                                                                                                                                            AGPLTEIFSDIIANQNDR-YLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB0384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U49938; AAC44711.1; -.-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE001143; AAC66756.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003760;
                                                                                                  1 (Rel. 40, Created)
1 (Rel. 40, Last sequ
1 (Rel. 40, Last anno
Lipeptidase B (EC 3.4.
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353
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17 N
179 V
39824 MW;
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23.7%;
                                                                Bacillus/Clostridium
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V -> L (IN STRAIN 297).
; 2E8FF607D6CAB9B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 147;
Pred. No. 0.
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                                                                                                                                                                      PRT;
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                                                                                                                             update)
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M1;
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.027;
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                                                                                                                                                                                                                                                                                                                                        KEKGKAMALFMYKEDKVGVIFPI
                                                               group;
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                                                               Streptococcaceae;
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SCA4_RICFE
ID SCA4_R
AC Q9AJ37
DT 16-OCT
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SCA4_RICFE STANDARD;
O9AJ37;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Ferretti J.J., McS
Primeaux C., Sezat
                                                                                                             466
                                                                                                                                          445
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                                                                                                            SLD
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                                                                                                                                                                                                                                                                                                                                                                                                                     ASEDVEKVAKKAKSYTEVDGKFH---IAKSYNPPLNDANRSRSFSG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDNPAGEKWKDLSNGFEYPLPEHSYRYSAIPDVTPNKGVYDE------AGFNE-FGV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKFLGLGLVFPLSA--IATISAGCW----DKETTKE---------
                                                                                                                                          ITD
                                                                                                                                                                      ----VAAHPKPFGTKVIDEMK----GLEXTWIAEQDKSTKEISDLVVSDPKAAQEKADKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTGRYINLTYKTEEAGWLAGYANASFLAKKF--PSDPTKRSAIVIGGGISPAVTDFIAGY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNIVTLADKD-GIWYMEILSGHQYVA----IKFPDDKYAVFPNTFYLGHVDFNDKENTI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKYSSLANTNKNVW---VLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVI 181 | :||::| : :|: | || 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMS-ATVSASANDAIQKIDPYVKNGLAESSMTSVILPSVKTAREGVALIAKIVTEKGAAE
                                                                                                                                                                                                                                    SPRNAPYLPYLGNISRTYEAYQEKSTQYNDKS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----EKSADNON-------KQITDVSKISGLVNERKSEIMAAKADANKHFGL 78
                                                                                                                                                                                                     ADTSLEGNDKKLATEAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQPDKQQESLDKL
                                                                                                                                                                                                                                                                 KTKNKFFTSILKNLG--YSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDI 384
                                                                                                                                                                                                                                                                                              LDQMALDGKGKPKSKKAVKG----YAYPISNPNVMEAHIFQLKKDIPAELGGVMWLSIG
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                                                                                                            468
                                                                                                                                                                                                                                                                                                                                                          -- IKSLDPDSKVTYKDSNYELLQSTDKT-----FSLEDAMKLQRNRFEGLDLKP
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39 MW; B9394DC94C19AE4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NSFNOSSWEATQQLGALTGGE----ITSVDSSTAELE
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Best Local Similarity
Matches 108; Conserv
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sekeyova Z., Roux V., Raoult D.:
"Phylogenetic analysis of Rickettsia spp. by comparing t gene D coding for an intracytoplasmic protein.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rickettsia felis (Rickettsia azadi).
Bacteria; Proteobacteria; alpha subdivision;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Protein Page 14 OR D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Antigenic heat-stable 120 kba protein (PS12
(Protein PS 120) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
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GIYEGKANPEITSEKTKAV-SRGIDKSTAIPE--DKQALKDAANEAALDR
                                                                                                                                                                                                                                                                                          GITDAVIKSNLSTEDKGTMLIAVGDKVNASELSN---AEKQKLLGSVLKKGVEAQVLSPE 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAELEG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVFPLSAIAT------ISAGCWDKETTKEEKSADNQNKQITDVSK-ISGLVNERKSEI 65
                                                                                                                                             AEIKGETLESI----TKVVAESPLNGQDK
                                                                                                                                                                                                                   QQQLMQQNLDKITAEQTKNA----QITEVQGILANPAFNTIAKTEAIQNVTTKVLDSPIK
                                                                                                                                                                                                                                                       VTDFIAGYLAGIKAWNLKNSDKKTKIT-TDKIEINLGFD------VQDTSTKERLEQIA 283
                                                                                                                                                                                                                                                                                                                              --TGRYINLTYKTEEAGWL----AGYANASFLAKKFPSDPTKRSAIVIGGGI-----SPA 231
                                                                                                                                                                                                                                                                                                                                                                                                    KYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIP---
                                                                                                                                                                                                                                                                                                                                                                                                                                         --AEKQAN-----IIALTENTVNNNDLTPDTKVA----GVNAVLETIKNDQNTPDLE- 489
                                  AISEAKKEFE---EKTKTIPAEEVRKTLEIPEMPDKQPDK---QQESLDK 443
                                                                                                      VFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLAT----E
                                                                                                                                                                               SKDKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYS 343
                                                                                                                                                                                                                                                                                                                                                                  -KSKMLEATVAIALNSENGE------PKQKQQMLEKAVDV-GLSLKDDASRVTAID 537
                                                                      -----ASHKTMAPTEKISTIESVEKGVAESITDL-----EDKKLMTKGLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               981 AA;
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23.0%;
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; Pred. No. 0.84;
71; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7F18F421E2C262E1 CRC64;
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(PS120)
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Search completed: July 18, 2002, 15:30:19 Job time: 66 sec

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US-09-308-347-36

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US-08-923-992A-4

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US-08-409-995-4

US-08-685-467-4

US-08-913-942-4

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4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4 .8	4.8	4.8
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US-09-074-658-15	US-08-447-031A-2	US-08-867-941-15	US-08-646-273-36	US-08-646-273-25	US-08-235-836C-72	US-09-336-447A-9	US-08-235-836C-68	US-08-913-942-6	US-08-685-467-6	US-08-409-995-6	US-08-755-587-184	US-08-790-912-2	US-08-790-912-3	US-08-923-992A-10	US-08-923-992A-6	US-09-268-347-44	US-09-669-974-32
Sequence 15, Appl	2	15,	Sequence 36, Appl	Sequence 25, Appl	Sequence 72, Appl	٥	5	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 184, App	Sequence 2, Appli	ω `	Sequence 10, Appl	Sequence 6, Appli	Sequence 44, Appl	Sequence 32, Appl

ALIGNMENTS

;; TYPE: amino acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-961-083-8 RESULT 1 US-08-961-083-8 Sequence 8, Application US/08961083 Patent No. 6159469 GENERAL INFORMATION: TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 8: REFERENCE/DOCKET NUMBER: PB TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452 CORRESPONDENCE ADDRESS: SEQUENCE CHARACTERISTICS: LENGTH: 328 amino acids FILING DATE: ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, CURRENT APPLICATION DATA: COMPUTER: HE VELLE MSDOS OPERATING SYSTEM: MSDOS COFTWARE: ASCII Text DATA: NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, CLASSIFICATION: 435 APPLICATION NUMBER: FILING DATE: COUNTRY: STATE: STREET: 9410 Key West Avenue CITY: Rockville ADDRESSEE: 20850 Maryland USA Choi et. HP Vectra 486/33 Human Genome Sciences, al. US/08/961,083 36,373 3.50 inch, 1.4Mb version 6.2 PB340P2 storage

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61 RKSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQOLGA---LTGGEITSVD 117

Query Match Best Local S Matches 98

y Match 8.8%; Sco Local Similarity 25.7%; Pro hes 98; Conservative 56;

Score 203; DB 4; Length 328; Pred. No. 1.5e-10; Mismatches 144; Indels 84;

Gaps

19;

Length 328

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                 TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/487,716
FILING DATE: 05-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                          REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 05-MAY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/020,245 FILING DATE: 19-FEB-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 01-MAR CLASSIFICATION: 435
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STATE: NEW YOR
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                                                                       (212) 751-6849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLOPPY DISK
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01-MAR-1995
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; IDENTIFICATION METHOD:
; OTHER INFORMATION: p39a protein sequence
US-08-396-957A-5
                                                                                                                                                                                                                                          Sequence 4, Application US/08396957A Patent No. 5780041
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                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: SIMPSO
COMPUTER READABLE FORM:
                                                                                                          NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: p39a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                           413 KTIPAEEVRKTLEIP 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 A-----VVFRVEQGAFLAGYIAAKKSFSGK-----
                                                                                                                                                                                                                                                                                                                                                        311 KVLERKIVNKEIIVP 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 TKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 AAGLAGIGVIEAAKNLGDGYYVIGADQDQS--YLAPKN-FITSVIKNIGDALYLITGE-Y 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 --LANTNKN----VWVLSGFQHGDAFTRWLKIPENKQLFTEKNII--ILGIDWTDTENVI 181
                             COUNTRY:
                                                        CITY: NEW YORK STATE: NEW YOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 SDLDNLKRNGSDLIW-LVGYMLTDA--SLLVSSENPKI--SYGIIDPIYGDDVQIPENLI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Borrelia burgdorferi STRAIN: Sh-2-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 SSKKIKISMLV---DGVLDDKSFNSSANEALLRLKKDFPENIEEVFS--CAISGVYSSYV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 7.8%;
Local Similarity 26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANELLE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                IKNNNV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGYESGAKYAN-KDIEIISEYSNSFSDVDIG------RTTASKMYSKGIDVIHF 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASK--DKPSTLLAV 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGPLTEI-FSDIIANOND-RYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDLY 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTGRYINLTYKTEEAGWLAGY -- ANASFLAKKFPSDPTKRSAIVIG -- GGISPAVTD-FI 236
                     10154
                                                    NEW YORK
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                                                                                         345 PARK AVENUE
                                      USA
                                                                                                                                                                SIMPSON, WARREN; SCHWAN, TOM G. VENTION: ANTIGENIC PROTEINS AND VENTION: GENES ENCODING SAME OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                ---WEGGK----VVQMGLRDGVIGLPNAN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 179; DB 1;
Pred. No. 2.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123; Indels
                                                                                                                                                                  BORRELIA BURGDORFERI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----IGFIGGMKGNIVDAFR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 341;
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Gaps

MEDIUM TYPE:

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/664,731
APPLICATION NUMBER: 05-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 08/020,245
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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REFERENCE/DOCKET NUMBER: 20:
IELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
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189
                                                                  143
                                                                                    202 YANASFLAKKEPSDPTKRSAIVIGGGISPAVTD-FIAGYLAGIKAWNLKNSDKKTKITTD 260
                                                                                                                                                                     143
                               261 KI----EINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIANQ--NDRYL 314
                                                                                                                                   93
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                                                                                                                                                                                                                                    87
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OTHER INFORMATION: se
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE:
CELL LINE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN: Sh-2-82
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YIGSFADLEAGRSVATRMYSDEID-----IIHHAAGLGGIGAIEVAKELGSGHYI 238
                                                                  YIAAKL---
                                                                                                                                  YRESDVAKVAALQNPDMKYAI------IDPIYSNDPIP-ANLVGMTFRAQEGAFLTG
                                                                                                                                                                FQHGD-AFTRWLKIPENKQLFTEKNIIILGIDWTDTENVIPTGRYINLTYKTEEAGWLAG
                                                                                                                                                                                                 GTFDDKSFNESALNGVKKVKEEFKIELVLKESSSNSYLSDLEG----LKDAGSDLIWLIG
                                                                                                                                                                                                                                  GTVNDNSFNQSSWEAIQQLGALTGGEITSVDSST----AELEGKYSSLANTNKNVWVLSG 142
                                                                                                                                                                                                                                                                      85; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339
                                                                                                                                                                                                                                                                7.0%; Score 162; DB 1; Length 339; ilarity 22.8%; Pred. No. 9.2e-07; Conservative 69; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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05-MAY-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                               -SKTGKIGFLGGIEGEIVDAFRYGYEAGAKYAN-----KDIKISTQ 188
                                                                                                                                                                                                                                                                                                                                                                   sequence.
                                                                                                                                                                                                                                                                                                                                                                                        p39' protein
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                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 716-263-1600 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION: 716-263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                      128 SSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIIILGI----DWTDTENVIPT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 -SNKESYEKFLKE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239
140 NS-LAIKFRNEEAAFLAGYIAAKMSRKE------KIGFLTGPMSEHLKDFKFGFK 187
                                   184 GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIG---GGISPAVTDFIAGYL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       435 DKQQESLDKLITD
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                                                                        92 EVQKNPLNLFWLI-GYRFSDL-----SVKLSYERPDIYYGIIDAFDYGDIQ--VPK 139
                                                                                                                                                   34 VLAHGSFYDKGYNQSVHDGVVKLRDNFGIKLITKSLRPYPIEGKRLLTVDE--AMTEDAY 91
                                                                                                                                                                                     83 VTAGGTVNDNSFNQSSWEAIQQLG------ALTGGEITSVDSSTAELEGKY 127
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Nixon, Hargrave, Devans & Doyle P.O. Box 1051, Clinton Square
                                                                                                                                                                                                                                                                                                                                                                                                               353 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          716-263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schwartz Ph.D., Ira
VENTION: Chromosomally-Encoded Membrane
VENTION: Protein of Borrelia Burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cabello M.D., Felipe
Godfrey M.D., Henry P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aron
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                          single
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                                                                                                                                                                                                                          Score 144; DB 4; I
Pred. No. 4.4e-05;
4; Mismatches 131;
                                                                                                                                                                                                                                                              Length 353;
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US-09-336-447A-15
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CURRENT FILING DATE: 1999-06-21
NUMBER OF SEO ID NOS: 98
SOFTWARE: PATENTIN VET. 2.1
SEO ID NO 15
LENGTH: 889
TYPE: PRT
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Best Local
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APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF
FILE REFERENCE: AMCY:024
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APPLICANT: HANSEN, ERIC J
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EAIDALNKASSENTQNI - - EDLAAYNELQDAYAKQQTEAIDALNKASSENTQN
                                  EAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPDKQPDKQQESLDKLITDINKN
                                                                      KADLTKDIKALESNVEEGLLDLSGRLIDQKADIAQN--QANIQDLAAYNELQDQYAQKQT
                                                                                                         KSN-SRNLAGFEFGKKSATVYLG--IKDRFVDIADTSLEGNDKKLA------T
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COPE, LESLIE D.
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GENERAL INFORMATION:

APPLICANT: DAUBERSIES, PIERRE

APPLICANT: DAUBERSIES, PIERRE

APPLICANT: DAUBERSIES, PIERRE

ITILE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STITLE REFERENCE: 0660-0125-0 PCT

CURRENT APPLICATION NUMBER: US/08/973,462B

CURRENT FILING DATE: 1998-02-06

EARLIER APPLICATION NUMBER: PCT/FR96/00894

EARLIER APPLICATION NUMBER: FR 95/07007

EARLIER APPLICATION NUMBER: FR 95/07007

EARLIER APPLICATION NUMBER: ST 95/07007

EARLIER APPLICATION NUMBER: ST 95/07007

EARLIER FILING DATE: 1995-06-13

NUMBER OF SEQ ID NOS: 29
US-09-308-375-2
, Sequence 2, Application US/09308375
, Patent No. 6300117
, GENERAL INFORMATION:
, APPLICANT: Genencor International,
, TITLE OF INVENTION: Proteases From
, FILE REFERENCE: GC394-PCT
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Best Local Similarity
Matches 85; Conserv
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TYPE: PRT
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                      Inc.
Gram-Positive Organisms
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                                                                                                                                                                                                                     us-09-268-347-36
     APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE
FILE REFERENCE: 1038-860
CURRENT APPLICATION NUMBER: US/09/268,347
CURRENT FILLING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54
SOFTMARE: PATENTIN Ver. 2.0
SEQ ID NO 36
SEQ ID NO 36
                                                                                                                                                             Sequence 36, Application US/09268347 Patent No. 6335182 GENERAL INFORMATION:
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LENGTH: 2285
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Best Local Similarity
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CURRENT FILING DATE: 1999-05-14
EARLIER APPLICATION NUMBER: EP9719636.4
EARLIER FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 2411
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                                                                                                                                                                                                                                                                                                                                                                                                            EAKKEFEEKTKTI--PAEEVRKTLEIPEMPDK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLLAAVSTATLLLSK--NTRTLASSLILGTRAMGQETLATAGLEAGMTRAAVASRVLKT
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                                                                                                                                                                                                                                                                                                  QSDI 938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-923-992A-4
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Best Local Similarity 20.8%;
Matches 108; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tai, Joseph Y.
APPLICANT: Blake, Milan S.
TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of
TITLE OF INVENTION: Streptococcal Beta Antigens
                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.
STREET: 1100 New York Avenue, N.W., Suite 600
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478
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                                     APPLICATION NUMBER: FILING DATE: 05-SEF CLASSIFICATION: 536
                                                                                                                                                                                                                                                            STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                     COUNTRY:
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                                           05-SEP-1997
N: 536
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                                                                            US/08/923,992A
  US 60/024,707
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Pred. No. 0.1;
                                                                                                                     Version
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US-08-790-912-4
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REGISTRATION NUMBER: 32,893
REFERENCE, DOCKET NUMBER: 1438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
TYPE: MAINO acids
TYPE: MAINO acids
TYPE: TYPE: TOTALE TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08790912
Patent No. 5976542
GENERAL INFORMATION:
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT TITLE OF INVENTION: OF STREPTOCCOCCUS PNEUMONIAE INFECTION NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:

ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: 1601 Market Street, 36th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Weiser, Jeffrey
APPLICANT: Plaut, Andrew G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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                                                                              ZIP: 19103-2398
                                                                                                         COUNTRY:
                                                                                                                                                      STATE:
                                                                                                                                                                                       CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
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                                                                                                                                              Pennsylvania
                                                                                                                    USA
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; MOLECULE TYPE:
US-08-790-912-4
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ATTORWEY/AGENT INFORMATION:
NAME: Leary, Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 7600-401
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 167-2020
TELECOMMUNICATION 167-2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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SEQUENCE CHARACTERISTICS:
                                                                           1696
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1756 FKKAMYEERKNKFDSLNKVTFDDTRQPWTSYATKTISTVEELQTL 1800
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CURRENT APPLICATION DATA:
                                      404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 VFPLSAIATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNERKSEIMAAKADANKH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (215) 567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 29-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60 FILING DATE: 23-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                           ELLAAKGFKDGMVPYISNQYEDDAKQNGKTISIYGKTRGLVTDDLVLRKVFNGQFNNWTE
                                                                                                                  VYL---GIKDRFVDIADT---
                                                                                                                                                                                                                                                                                                                                            LKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDIIA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDYWYRIL------DEQGREKLYRNILVYDAYKFGDDTTVDKATVEAQ------ 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFVISTISSLGFGAYDRYRNNEHRAGAELNK------FVEDNAQETAKRQRD---H 1401
                                    AKKE-FEEK----
                                                                                                                                                       QKLNSFNSLIENDILSAREYKNGDVERNGYHTIKLFSPIYSALSSEKGTPGDLMGRRIAY 1695
                                                                                                                                                                                                                                                                                                           APDHPDDATITVNSI---LKYDKNDASEKSRLQVL----DPTKRFQNADDL----KNYVH 1575
                                                                                                                                                                                                                                                                                                                                                                                           EMTHDSDNEIYLGGYGRRSGLGPEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                NLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGIKAWN 247
                                                                                                                                                                                           ------GYSVFSVLSDLYTKKSNSRNLAGFEFGKKSAT 372
                                                                                                                                                                                                                                  NMFDVIYMLEYLEGMSIVNRLSDVQKVNALRKIENKYVRDADGNDVYATNVIKNITMADA 1635
                                                                                                                                                                                                                                                                         NQND-----RYLIGV------DTDQSLVYTKTKNKFF------TSILKNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVWVLSGFQHGDAFTRWL------KIPENKQ--LFTEKNIIILGIDWTDTENVIPTGRYI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAELEGKYSSLANTNK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                831-494
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Pred. No. 0.1
                                    -----TKTIPAEEVRKTL 424
                                                                                                              ----SLEGNDKKLATEAI-----SE 403
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US-09-336-447A-5

Sequence 5, Application US/09336447A Patent No. 6310190

CORRESPONDENCE ADDRESS:

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US-09-074-658-75
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                                                                                                                                                  Sequence 75, Application US/09074658 Patent No. 6184371 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 892
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APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBL, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.2%; Score 119; DB 4; Length 892; Rest Local Similarity 20.8%; Pred. No. 0.039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atches 105;
APPLICANT: Run-Pan Du
APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES
                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                          424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 STIGGGYYNQATGEKSTVAGGRNNQATGNNSTVAG------GSYNQATGNNST 192
                                                                                                                                                                                                                                                                                                                                                                                                   371 -ATVYLGIKDRFVDIAD----TSLEGNDKKLATEAISEAKKEFEEKTKTIPAEE--VRKT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 IVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVLS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 ATISAGCWDKETTKEEKSADNQNKQIT-DVSKISGLVNERKSEIMANKADANKHFGLNMA
                                                                                                                                                                                                                                                                                                                          LEIPEMPDKQPDKQQESLDKLITDI 448
                                                                                                                                                                                                                                                                                                                                                                TAKNQADTAQNQTDIQDLAAYNELQDQYAQKQTEAIDALNKASSANIDRIATAELGIAEN
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                                                                                                                                                                                                                                                                                        KKDAQIAKAQANENKDGIAKNQADI 599
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                                                                                                                                    Loosmore,
                                                                                                                                    Sheena M
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                                         MORAXELLA
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                                                                                                                                               RESULT 13
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  Sequence 4, Application US/08409995
Patent No. 5646259
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen I
APPLICANT: St. Geme III, JOSeph
TITLE OF INVENTION: Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.1%; Score 117.5; DB Best Local Similarity 19.5%; Pred. No. 0.058; Matches 79; Conservative 68; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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CITY: Toronto
STATE: Ontario
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                                                                                                                                                                                                                                        337 LKNLGYSVFSVLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRF
                                                                                                                                                                                                                                                                                541 ----ASKAVSRPEQLSHNAARISE-FSDYADDGKYKYLLGK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 KONKKAEYFLAEGESELKPAAKLAGNGNYLKNOLNRWVEERKKNNOSLSAEEEAMVREAO 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 KETTKEEKSADNONKOITDVSKISG------LVNERK------SEIMAAKAD
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                                                                                                                                                                                                       VEG---SVCGYIETLRSRKCVPRKING-----SNIHISLNDRF
                                                                                                                                                                                                                                                                                                                       LEQIASK--DKPSTLLAVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSI 336
                                                                                                                                                                                                                                                                                                                                                                 ACRASADKPYSYDSSDRFHYREQHNVLNALFEKSLKNKWTKHHLTLGFGYD------
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    T: Barenkamp, Stephen I.
T: St. Geme III, Joseph
INVENTION: Haemophilus
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Haemophilus
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Adhesion
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; STRANDEDNESS: dou
; TOPOLOGY: unknown
US-08-409-995-4
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Best Local S
Matches 109
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,995
FILING DATE: 24-MAR-1995
CLASSIFICATION:
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
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NAME: Silva, Robin M.
REGISTRATION UNMBER: 38,304
REFERENCE/DOCKET NUMBER: A-61053/RFT
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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LENGTH: 1912 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
737 TFVKTENLTTSIDEDNPTDNGKDDALKAGDTLTFKAGKN
                                     413 KTIPAEEVRKTLEIPEMPDKQPDKQQESLDKLITDINKN 451
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Local Similarity 21.0%; Pred. No. 0.2;
hes 109; Conservative 65; Mismatches 217;
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TELEFAX: (415) 398-3249
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                                                                                                                       KKSNSRNLAGFEFGKKSATVYLGIKDR-FVDIADTSLEGNDKKLATEAISEAKKEFEEKT
                                                                                                                                                                                                      ANQNDRYLI------GVDTDQSLVYTKTKNKFFTSILK--NLGYSVFSVLSDLYT 353
                                                                                                                                                                                                                                                                                           KKTKITTDKIEI-----NLGFDVQ-DTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDII 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSFNQSSWEAIQQLGALTGGEITSVDSSTAELEGKYSSLANTNKNVWVL---SGFQHG-- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAFTRWLKIP-----ENKQLFTEKNIIIL-----GIDWTDTENVIPTGRYINLTYK 192
                                                                                                                                                                                                                                                                                                                                    TNVASGLRAYDDANF-----DVLNNSATDLNRHVEDA-----YKGLLNLNEKNAN
                                                                                                                                                                                                                                                                                                                                                                                                                     DALTGLTSITLGGTTNGGNDAKTVINKDGLTITPAGNGGTTGTNTISVTKDGIKAGNKAI 538
                                                                              K-----GGFETVKTGAT----DADRGKVTVKDATANDADKKVAT--VKDVATAINSAA 736
                                                                                                                                                               -SENGKHTITVSVAETKADCGLEKDGDTIKLKVDNQNTDNVLTVGNNGTAV-----T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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APPLICANT: Barenkamp,
TITLE OF INVENTION: HI
NUMBER OF SEQUENCES: (
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LENGTH: 1912 amino acids
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REFERENCE/DOCKET NUMBER: A-61053-2/RFT/RMS
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION UNMEER: US/08/685,467 FILING DATE: 22-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                               539 TNVASGLRAYDDANF------DVLNNSATDLNRHVEDA------YKGLLNLNEKNAN 583
                                                                                                                                                                                        147
                                                                                                                                                                                                                                422 TALGNISWKA--KAEADTDGALEGI-SKDQEVKAGETVTFKAGKNLKVKQDGANFTYSLQ 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 GLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQI-----TDVSKISG-----LVN 59
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    KKTKITTDKIEI-----NLGFDVQ-DTSTKERLEQIASKDKPSTLLAVAGPLTEIFSDII 306
                                                                                                                                        DALTGLTSITLGGTTNGGNDAKTVINKDGLTITPAGNGGTTGTNTISVTKDGIKAGNKAI 538
                                                                                        TEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGIKAWNLKNSD 252
                                                                                                                                                                                   DAFTRWLKIP-----ENKQLFTEKNIIIL-----GIDWTDTENVIPTGRYINLTYK 192
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Sequence 33, Application US/09377155
Patent NO. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
APPLICANT: MOXON, E. Richard
FILE REFERENCE: 065064/0128
CURRENT APPLICATION: UNMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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; TYPE: PAT
; ORGANISM: Haemophilus influenzae
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SEQ ID NO 33
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Search completed: July 18, 2002, 09:14:54 Job time: 34 sec

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2: sp_bacteria
3: sp_fungl:*
4: sp_human:*
5: sp_inverteb;
6: sp_mammal:*
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8: sp_organel1
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
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13: sp_verteb;
14: sp_unclass:
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Gapop 10.0 , Gapext 0.5
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1 MKKKIKWNKFLGLGLVFPLS......KQPDKQQESLDKLITDINKN 451
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Q98q15 mycoplasma
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Q52311 mycoplasma
Q9rgx5 mycoplasma
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Q99zh4 streptococc
Q90zh0 streptococc
Q90zh0 streptococc
Q90zh0 lactococcus
Q97160 clostridium
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Q9ajr8 erysipeloth	Q91962 moraxella c	N)	ש	Q926d6 rhizobium m	Q9xd52 moraxella c	Q9rsq4 deinococcus	Q91961 moraxella c	Q9pq10 ureaplasma	Q46239 clostridium	borrelia	borrelia	σ	Q98gw4 rhizobium l	Q9r777 borrelia bu	borrelia	borrelia	087960 borrelia bu	σ	9	S		borrelia	borrelia b		Q9wxv7 thermotoga	Q9ak41 streptomyce	Q9a1p7 streptococc	Q9prd3 ureaplasma

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ALIGNMENTS

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Matches 140; Conserv
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STRALM-UAB CTIP;
MEDLINE-21267165; PubMed-11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Sa
Moszer I., Dybvig K., Wroblewski H., Viari A.,
Blanchard A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q98QL5;
                                                                                                                                                                                                              "The complete genome sequence of the murine Mycoplasma pulmonis.";
Nucleic Acids Res. 29:2145-2153(2001).
EMBL; AL445564; CAC13519.1; -.
MypuList; MYPU_3460; -.
InterPro; IPR003760; Bmp.
Pfam; PF02608; Bmp; 1.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
ABC TRANSPORTER XYLOSE-BINDING LIPOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasmataceae;
NCBI_TaxID-2107;
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Mycoplasma pulmonis.
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 TS.
                       VTETQKIVENKIKQASLETQK-----VVLITADGNIDDKSENQQVYESQKTLKDFVDKAY 106
                                                                           MKLNK--KLFSILPVAALAIALPATF-----VSCAQNPNKTNSNLDSSKITDLLSQKE
                                                                                        ANPT-NYKSVLGIPTMLINDNDAKDNEKASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRNLAGFEFGK----KSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKKEFEEKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSVVDAIKKSNKDTKYLIGVDTDQSKIFSPA-TVFFTSIEKHLGRTIYQVLTDIWLKKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIFSDII--ANQNDRYLIGVDTDQSLVYYKTKNKFFTSILKNLGYSVFSVLSDLYTKKSN
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                                                                                                                                                                                         proteome.
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                       KSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEI 113
                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma
                                                                                                                                                                                         51096 MW;
                                                                                                                                       24.18;
VDSSTAELEGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENK 159
                                                                                                                          ; Score 554.5; DB 16;
; Pred. No. 4.1e-24;
88; Mismatches 175;
                                                                                                                                                                                         6724D4D820809CE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439
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                                                                                                                                                                                                                                                                                           respiratory
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                                                                                                                                                    461;
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                                                                                                                                                                                                 Query Match
Best Local S
Matches 141
                                                                                                                                                                                                                                                                    CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                             Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                               malp product of Mycoplasma ferment of bacterial lipoproteins... Infect. Immun. 67:6213-6216(1999). EMBL: AJ132423; CAB43718.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09x//2;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
v44 MEMBRANE LIPOPROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                     InterPro; IPR003760; Bmp. Pfam; PF02608; Bmp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycoplasma agalactiae.
Bacteria; Firmicutes;
Mycoplasmataceae; Myco
                                                                                                                                                                                                                                                                                                                                                                                                                     Pittau M.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20002620; PubMed=10531294; Rosati S., Pozzi S., Robino P., Montinaro B., Conti A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-M7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9X775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9X775
                                                                                                                                                                                                                                                                                                                                                                                                    "P48 major surface antigen of Mycoplasma agalactiae is
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20002620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2110;
             169
                                        108
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                                       NLRNKVYEPKKGQLLEAYKNAIDSGFRYIVLCGFTHQASL---VGLDENYIKKIKDNNII
                                                                                                                                              KKNKFYLFLGAA----PVLSVPLVAASCGDKYFKETEVDGVKTISTLAHITSRKGLKLREG
                                                                                                                                                                        KKIKWNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQITDVSKISGL-VNER
             ILGIDWT---
                                                                  ELEGK----
                                                                                                                     KSEIMAAKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTGGEITSVDSSTA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSRVKESIKTQADTSIQKAIDKWNANPNSKKIEKEMTNGDLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSILKNLGYSVFSVLSDLYT------KKSNSRNLAGFEFGKKSATVYLGIKDRFVDIA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSAIVIGGGISPAVTDFIAGYLAGIKAWN--LKNSDKKTKITTDKIEINLGFDVQDTSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QLETEKNIIILGIDWTDTEN-VIPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTK 218
                                                                                           LTVENAPKA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVVSNVVETGKSTISLPVAGPFTGVVVDVLRKDTSDEDRFIVGVDTDQSLSFTNDSKRFF
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                                                                                                                                                                                                                                                                                                          Lipoprotein.
                                                                                                                                                                                                                                                                   23
465 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.A.
                                                                                                                                                                                                                                                                    AA;
             DTENV----
                                                                                                                                                                                                                                                                 22
465 P
51149 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma
                                                                                                                                                                                                              18.1%;
                                                                                         ---TFITDEGSVHDESFNQSGWEAVHKVSYELGLDKAQV-SGNK 107
                                                              YSSLANTNKNVWVLSGFQHGDAFTRWLKIPENK-QLFTEKNII 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus/Clostridium
                                                                                                                                                                                                   94;
             IPTGRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTK
                                                                                                                                                                                                                                                                                                                                                                                         termentans
                                                                                                                                                                                                              Score 417; DB 2;
Pred. No. 3.1e-16;
                                                                                                                                                                                                                                                                   P48 MEMBRANE LIPOPROTEIN.
60AD5448CFE03C96 CRC64;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrembLrel. 06, 01-JUN-1998 (TrembLrel. 06, 01-JUN-2001 (TrembLrel. 17, MEMBRANE LIPOPROTEIN P48V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipoprotein SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasmataceae;
NCBI_TaxID=2115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma fermentans.
Bacteria; Firmicutes; Bacillus/Clostridium
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EMBL; AF099211; AAD16395.1; -.
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01-UN-2001 (TIEMBLIEL. 17, Last annotation update)
MACROPHAGE ACTIVATING LIPOPROTEIN-404 PRECURSOR.
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EMBL; D64083; BAAA2530.1; -.
EMBL; AB026157; BAA77211.2; -.
InterPro; IPR003760; Bmp.
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Nagasawa S., Akedo H., Seya T.;
"A novel protein that participates in nonself discrimination
malignant cells by homologous complement.";
Nat. Med. 3:1266-1270(1997).
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  -DESKRVVASFGGGAFPGVTTFNEGFAKGI
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Best Local S
Matches 128
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NCBI_TaxID=2101;
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01-MAY-2000
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                                                                                                                                               GRYINLTYKTEEAGWLAGYANASFLAKKFPSDPTKRSAIVIGGGISPAVTDFIAGYLAGI 243
                        LYYNQKH--KSSKIYHTSPVKLDSGF
                                                                  KAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS------KDKPSTLL
                                                                                                                    --FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVASFGGGAFPGVTTFNEGFAKGI
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"Differential posttranslational processing confers intraspect
variation of a major surface lipoprotein and a macrophage-act
lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-771(1999).
EMBL; AF099210; AAD16394.1; -.
InterPro; IPR003760; Emp.
Pfam; PF02608; Emp; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MACROPHAGE ACTIVATING LIPOPROTEIN-404 PRECURSOR.
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                                                                                                        VVKNAEL-----LKLKPVLITDEGKIDDKSFNQSAFEALKAINKQTGIEINNVEPS-SNF 106
                                                                                                                                                                                                             MKKSKKILLGL-SPIAAILPAVAVSCGNNDES-----NISFKEKDISKYTTNANGKQ
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ESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREELERNQIKIIGIDF-DIETEYKW 163
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                                                                                                                                                                                                                                                                                                                   Score 394; DE
Pred. No. 5.8e
)1; Mismatches
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MACROPHAGE ACTIVATING LIPOPROTEIN-404.

B6D09a8812AC3171 CRC64;
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"Differential posttranslational processing confers intraspeci-
variation of a major surface lipoprotein and a macrophage-act
lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-771(1999).
EMBL, AF099212; AAD16396.1; -.
ToterPro; IPR003760; Bmp.
Pfam; PF02608; Bmp; 1.
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Bacteria; Firmicutes; Bacillus/Clostridium
Mycoplasmataceae; Mycoplasma.
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01-MAY-2000 (TrEMBLrel. 13, Last sequinous control (Tremburel. 17, Last annown MACROPHAGE ACTIVATING LIPOPROTEIN-404
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                       IKWNKFLGLGLVFPLSAI-ATISAGCWDKETTKEEKSADNQNKQITI)VSKISGLVNERKS
                                                              LYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVINNVLSBTPADVKYNPHVIL
                                                                                                                                                                                           VVKNAEL-----LKLKPVLITDEGKIDDKSFNQSAFEALKAINKQTGIEINNVEPS-SNF
                                                                                                                                                                                                                                     MKKSKKILLGL-SPIAAILPAVAVSCGNNDES-----NISFKEKDISKYTTINANGKQ
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                                   AVAGPLTEIFSDI-IANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDL
                                                                                    KAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS-------KDKPSTLL
                                                                                                        --FYSLQFNIKESAFTTGYAIASWLSEQ----DESKRVVASFGGGAF);GVTTFNEGFAKGI
                                                                                                                                                  ESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREELERNQIKIKGIDF-DIETEYKW
                                                                                                                                                                       EGKYSSLANTNKNVWVLSGFQHGDAFTRWLKIPENKQLFTEKNIII).GIDWTDTENVIPT
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                                                                                                                                                                                                                                                                                   127;
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                                                                                                                                                                                                                                                                                           Similarity
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429 /
                                                                                                                                                                                                                                                                                  Conservative
                    FETVRLAANKGQYVIGVDSDQGMI--QDKDRILTSVLKHIKQAVYETLLDL
YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEA
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                                                                                                                                                                                                                                                                                                                                     429
47933
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27.0%;
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Last annotation update)
ROTEIN-404 PRECURSOR.
                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                    POTENTIAL.

MACROPHAGE ACTIVATING LIPOPROTEIN-404

; B6D08CF975AC3171 CRC64;
                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KEKWIGVAENHFSNTEEQAKINNK
                                                                                                                                                                                                                                                                                           394;
No. 5
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                                                                                                                                                                                                                                                                                         DB 2;
.8e-15;
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                                                                                                                                                                                                                                                                                                     Length 429;
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Query Match
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"Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopeptide of Mycoplasma fermentans.";
Infect. Immun. 67:760-771(1999).
EMBL; AF099209; AAD16393.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TIEMBLIEL 13, Created)
01-MAY-2000 (TIEMBLIEL 13, Last sequence update)
01-JUN-2001 (TIEMBLIEL 17, Last annotation update)
MACROPHAGE ACTIVATING LIPOPROTEIN-404 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Lipoprotein.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003760; B
Pfam; PF02608; Bmp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycoplasma fermentans.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99115554; PubMed=9916088;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9RGX7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKKIKWNKFLGLGLVFPLSAIATISAGCWDKETTKEEKSADNQNKQITDVSKISGLVNE
                  EAISEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDINK
                                                             DLILEKEEGYKPYVVKDKKADKKWSHFGTQ-----KEKWIGVAENHFSNTEEQAKIN
                                                                                                                                                  VILSVAGPAT - - FETVRLANKGQYVIGVDSDQGMI - - QDKDRILTSVLKHIKQAVYETLL
                                                                                                                                                                             TLLAVAGPLIEIFSDIIANQNDRYLIGVDIDQSLVYTKTKNKFFTSILKNLGYSVFSVLS
                                                                                                                                                                                                                                    KGILYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVINNVLSSTPADVKYNPH
                                                                                                                                                                                                                                                                  AGIKAWNLKNSDKXTKI-TTDKIEINLGFDVQDTSTKERLEQIAS------KDKPS
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                                                                                                                                                                                                                                                                                                                             YKW--FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVASFGGGAFPGVTTFNEGFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KQ---VVKNAELLK---LKPVLITDEGKIDDKSFNQSAFEALKAINKQTGIEINNVEPS-
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428 AA;
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                                                                                                      YTKKSNSRNLAGFEFGKKSATYYLGIKDRFVDIADTSLEGNDKKL-AT
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26.8%;
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Pred. No. 6.2e-15;
7; Mismatches 178;
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MACROPHAGE ACTIVATING LIPOPROTEIN-404.

; D6B69C0BA969CFE1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Best Loc
Matches
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Calcutt M.J., Kim M.F., Karpas A.B., Muhlradt P.F., Wise K.S.;
"Differential posttranslational processing confers intraspecies variation of a major surface lipoprotein and a macrophage-activating lipopeptide of Mycoplasma fermentans.";
Infect, Immun. 67:760-771(1999).
EMBL; AF099213; AAD16397.1; -.
InterPro; IFR003760; Emp.
Pfam; FP02608; Emp; 1.
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NCBI_TaxID=2115;
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Bacteria; Firmicutes; Bacillus/Clostridium
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01-MAY-2000
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Local Similarity
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                                                                                                         KEAIKMFKE---
                                                                                                                                                                                                                                                                                                                                AVAGPLTEIFSDIIANQNDRYLIGVDTDQSLVYTKTKNKFFTSILKNLGYSVFSVLSDL-:|||| | : : : : : : : : | : | | |
                                                                                                                                                SEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDINK
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                                                                                                                                                                                                                                                                                                                                                                                                      LYYNQKH--KSSKIYHTSPYKLDSGF----TAGEKMNTVINNVLSSTPADVKYNPHVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --FYSLQFNIKEPAFTTGYAIASWLSEQ---DESKRVVASFGGGAFPGVTTFNEGFAKGI
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illarity 26.8%;
Conservative 9
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                                                                                                                                                                                                                                                     YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEAI
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                                                                                                    LPEDFVKYINSDKALKDGNKIDNVSERLEAIISAINK
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Pred. No. 1e-14;
9; Mismatches 176;
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MACROPHAGE ACTIVATING LIPOPROTEIN-404;

C7A536B409A60132 CRC64;
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                                                                                                                                                                                                    -KEKWIGVAENHFSNTEEQAKINNKI
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RESULT
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Best Local S
Matches 125
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EMBL; AP009214; AAD16398.1; -.
EMBL; AP099214; AAD16398.1; -.
EMBL; AP099215; AAD16399.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000
01-MAY-2000
01-OCT-2001
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SEQUENCE
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SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2115;
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Bacteria; Firmicutes;
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MEDLINE-99115554;
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Local Similarity 26.6%;
hes 125; Conservative 10
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                                                                                                                                                                                                                                                                                                                               KAWNLKNSDKKTKI-TTDKIEINLGFDVQDTSTKERLEQIAS----
  KEAIKMFKE---
                                         SEAKKEFEEKTKTIPAEEVRKTLEIPEMPD-KQPDKQQESLDKLITDINK
                                                                                                                                                                                                                VVKNAEL-----LKLKPVLITDEGKIDDKSFNQSAFEALKAINKQTGIEINSVEPS-SNF
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                                                                                                                                                                                     SVAGPAT -- FETVRLANKGOYVIGVDSDQGMI--QDKDRILTSVLKHIKQAVYETLLDLI
                                                                                                                                                                                                                                                                                     LYYNQKH--KSSKIYHTSPVKLDSGF----TAGEKMNTVINNVLSSTPADVKYNPHVIL
                                                                                                                                                                                                                                                                                                                                                                                --FYSLQFNIKESAFTTGYAIASWLSEQ---DESKRVVASFGVGAFPGVTTFNEGFAKGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESAYNSALSAGHKIWVLNGFKHQQSIKQY--IDAHREELERNQIKIIGIDF-DIETEYKW 163
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(TrEMBLrel. 13, Last
(TrEMBLrel. 18, Last
MALP-404 PRECURSOR.
                                                                                                                                         -YTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKL-ATEAI
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-LPEDFVKYINSDKALKDGNKIDNVSERLEAIISAINK
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Pred. No. 1.4e
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MACROPHAGE ACTIVATING
59808324E218F03C CRO
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                                                                                             -KEKWIGVAENHFSNTEEQAKINNKI
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les 175;
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Q99ZH4; Q99ZH4; 01-JUN-2001

PRELIMINARY;

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PRT;

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RESULT
Q9EV91
ID Q9
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DT 01
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Best Local
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 Q9EV91;
Q9EV91;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam: PF00532; Peripla_BP_like; 1.
PROSITE; PS00227; TUBULIN; UNKNOWN_1.
Lipoprotein; Complete proteome.
SEQUENCE 350 AA; 36396 MW; 7B5A6A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an M1 strain of Streptococcus pyogenes. Proc. Natl. Acad. Sci. U.S. A. 98:4658-4663(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-SF370 / ATCC 700294 / SEROTYPE
MEDLINE-21192684; PubMed-11296296;
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01-DEC-2001 (TrEMBLrel.
PUTATIVE LIPOPROTEIN.
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                                                                                                                                                                                    VLSDLYTKKSNSRNLAGFEFGKKSATVYLGIKDRFVDIADTSLEGNDKKLATEAISEAKK 406
                                                                                                                                                                                                                                                                                                                        NVASVTFADHEAAYLAGIAAAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                               AKADANKHFGLNMAIVTAGGTVNDNSFNQSSWEAIQQLGALTG-GEITSVDSSTAELEGK
                                                                                                          KIKSGDIKVP
                                                                                                                                   EFEEKTKTIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KFIGLG----LASVAVLSLAACGNRG-----
                                                                                                                                                            INKQVADKK-----
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IPR003760; Bmp.
IPR001761; Peripla_BP_like.
IPR000217; Tubulin.
                                                                                                                                                                                                                                                                                                                                                                           TNLDTAVSGGYQLIYGIGFA--LKDAIAKAAGDNEGVKFVIID----DIIEGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
  (TrEMBLrel.
                                         PRELIMINARY;
                                                                                                                                   416
                                                                                                                                                                                                                                                                   ---VDDTIQVKVDYAGSFGDAAKGKTIAAAQYAAGAD--VIYQAAGGTG
                                                                                                                                                            --FPGGK--TTVY-GLKDGGVEIATT----NVSKEAVKAIKEAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.1%;
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19,
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16,
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Last annotation update)
Created)
Last sequence
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Pred. No. 7.
                                         PRT;
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                                                                                                                                                                                                                                                                                                                        ----TTKTKTVGFVGGMEGTVITRFEKGFEAGV
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7.7e-06;
hes 153;
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  update)
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Best Local Sim
Matches 112;
                                                                      Q97RH0
Q97RH0;
01-OCT-2001
01-OCT-2001
01-DEC-2001
Streptococcus.
NCBI_TaxID=1313;
                        SP0845.
Streptococcus pneumon
Bacteria; Firmicutes;
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MEDLINE=21089007; PubMed=11271425;
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                                                            LIPOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arch. Microbiol. 175:8-18(2001). EMBL; AJ276209; CAC14304.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular analysis of the grd-operon encoded proteins of the reductase and thioredoxinsystem from Clostridium sticklandii."
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(TrEMBLrel.
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                         Bacillus/Clostridium group; Streptococcaceae;
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Last sequence update)
Last annotation update)
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Pred. No. 1.1e
56; Mismatches
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Q9CFM9
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Best Local Similarity
Matches 110; Conserv
                    O9CFM9;
01-JUN-2001 (TremBLrel. 17, C
01-JUN-2001 (TremBLrel. 17, I
01-OCT-2001 (TremBLrel. 18, I
BASIC MEMBRANE PROTEIN A.
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SEQUENCE
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EMBL; AE007390; AAK74976.1;
TIGR; SP0845; -.
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Tettelin H., Nelson K.E., Palaisen I.T., Elsen J.A., Read T.D.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
HOltzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
Bolyberty B.A., Worrison D.A., Hollingshead S.K., Fraser C.M.;
"Complete genome sequence of a virulent isolate of Streptococcus
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SEQUENCE FROM N.A.
STRAIN-TIGR4;
                  BMPA
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InterPro; IPR000217; Tubulin.
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 Lactococcus
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PROSITE; PS00227; TUBULIN; UNKNOWN_1.
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350 AA;
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 lactis
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 lactis) (Streptococcus lactis).
                                           Last sequence update)
Last annotation updat
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Pred. No. 2
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Best Local Similarity 24.3
Matches 107; Conservative
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"The complete genome sequence of the lactic acid bacter lactis ssp. lactis IL1403.";
Genome Res. 11:731-753(2001).
EMBL; AE006374; AAK05536.1;
InterPro; IPR003766; Bmp.
Pfam; PF02608; Bmp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 350 AA;
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---DAVAKAKADIIDGKITVPSK
                      LATEAISEAKKEFEEKTKTIPAE
                                                                    KNLGYSVFSVLSDLYTKKSNSRNLAG--FEFGKKSATVYLGIKDRFVDIADTSLEGNDKK
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                                                 KEVG----NVVKDIADKTKDGKFPGGTIVTYDLKNGGVNLGL---
                                                                                                                VITRFEKGYEAGAKSVN------PDIKVDVQYAGSFSDAAKGKTIAAAMYGAGDDV
                                                                                                                                                                             AVTDFIAGYLAGIKAWNLKNSDKKTKITTDKIEINLGFDVQDTSTKERLEQIASKDKPST
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Pred. No. 0.000
62; Mismatches
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hes 156;
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